

RESULT	2	
ID	R04087	standard; protein; 134 AA.
AC	R04087;	
DE	01-JUN-1990	(first entry)
PR	Protein encoded by human natriuretic related peptide.	
KW	Porcine BNP; natriuretic; diuretic; vasodilator; hypertension.	
OS	Sus scrofa.	
FT	Key	Location/Qualifiers
FT	region	44..45
FT		/label=join between first and second exon
FT	region	130
FT		/label=join between second and third exon
PR	W08912069-A.	
PR	14-DEC-1989.	
PR	31-MAY-1989;	02373.
PR	31-MAY-1988;	US-200363.
PR	14-JUN-1988;	US-2006470.
PR	19-JAN-1989;	US-299880.
PR	(CALB) Calif Biotech Inc.	
PR	Sellhammer JJ, Lewicki J, Scarborough RM, Porter GJ;	
PR	WPI; 90-007453/01.	
DR	N-PSDB; 002852.	
PT	New natriuretic and vasodilator peptides - obtd. using cDNA sequence	
PT	encoding porcine brain natriuretic peptide and related human canine genes	
PS	Example 5; Fig.5; 6bp; English.	
CC	Sequences derived from porcine brain natriuretic gene can be used in part	
CC	as probes to isolate similar genes from different species. Although human	
CC	natriuretic related peptides (NRP) could not be isolated directly, canine	
CC	NRPs could be, and these could then be used as probes to their human	
CC	equivalents. Here the gene product is shown, taken from the plasmid	
CC	phbnp-1.	
SO	Sequence	134 AA;

Query Match	100.0%	Score 690	DB 1	Length 134
Best Local Similarity	100.0%	Pred. No. 8.1e-63		
Matches 134	Conservative	0	Mismatches 0	Indels 0
			Gaps	0

Qy	1	mdppgprsprallllllffhlaflgqrshpqlgspgsasdlertsqldqgrnhlgkrlselqve	60
Dd	1	MDPQAPSPALLLLFLHLAFLGGRSHPLGSPGSASDLETSGLQDGRNHLGKRLSELQVE	60
	61	qtslspqlgesprptgywvksrevateglgrhkrnlytlaprsppkmvqsgcfcgrkmdrl	120
Dd	61	QTSLEPLQGESPRPTGYWKSREVAETGIRGHRKKNLYTLRAPSPKMKVQSGCGGRKMDRI	120
Qy	121	ssssglgckvrlrrh	134
Dd	121	SSSSGLGCKVRLRRH	134

RESULT	3
ID	Y05325
AC	Y05325
DT	25-JUN-1999 (first entry)
DE	Human gamma-BNP protein sequence.
KW	Gamma-BNP; human; brain natriuretic protein; immunoassay; heart disease;
SW	cardiac insufficiency; diagnosis.
OS	Homo sapiens.
PN	WC0913331-A1.
PD	18-MAR-1999.
PR	11-SEP-1997; JP-246684.
PA	(SHIO) SHIONOGI & CO LTD.
PI	Asada H, Endou K, Shimizu H;
DR	WPI: 99-243746/20.
DR	N-PSDB: X33826.
PT	Sandwich Immuno assay for mammalian gamma BNP

CS Claim 2; Page 20-21; 24pp; Japanese.
PS This sequence is the human gamma-BNP (brain natriuretic protein).
CC This sequence is the human gamma-BNP (brain natriuretic protein).
CC The invention relates to an immunoassay method specific for mammalian
CC gamma-BNP derivatives, which comprises the use of a first antibody
CC reacting with mammalian alpha-BNP and a second antibody with prepro or
CC gamma-BNP derivatives but not with alpha-BNP. The immunoassay is useful
CC for diagnosing and monitoring heart diseases, particularly cardiac
CC insufficiency. The technique uses only blood plasma, and is simple,
CC stable and reliable.
SQ Sequence 134 AA;

Query Match	Best Local Similarity	Score	DB 1	Length
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0	100.0%;	690;	DB 1;	134;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0	100.0%;	Pred. No. 8.1e-63;		
Query 1	MDPQTAPSRALLLLFLHLAFGRSHPLGSPGSASDLETSLGQRNHLGKLSLAYE	60		
DB 1	MDPQTAPSRALLLLFLHLAFGRSHPLGSPGSASDLETSLGQRNHLGKLSLAYE	60		
Query 61	qtsleplqesprptvkwksrevategltghrkmvlytlraprpskmvgsgcfcgrkmdt	120		
DB 61	QTSLEPLQESPRPTVWKSREVATGIGHRKMVLYTLRAPRSPKMVGSGCFCGRKMDRI	120		
Query 121	ssssglgckvrlrrh	134		
DB 121	SSSSGLGCKVRLRRH	134		
RESULT 4				
ID R04084	standard; protein; 131 AA.			
AC R04084				
DT 01-JUN-1990	(first entry)			
DE Oligopeptide encoded by porcine brain natriuretic peptide cDNA.				
KW Porcine BNP; natriuretic; diuretic; vasodilator; hypertension.				
OS Sus scrofa.				
FT Key	location/qualifiers			
FT region	41..42			
FT /label=join of first and second exons.				
FT region	127			
FT /label=join of second and third exons.				
FT mat peptide	106..131			
PN W08912069-A.				
PN 14-DEC-1989.				
PF 31-MAY-1989; 02373.				
PR 31-MAY-1988; US-200383.				
PR 14-JUN-1988; US-2006470.				
PR 19-JAN-1989; US-299880.				
PR (CALB) Calif Biotech Inc.				
PI Sellhammer J; Lewicki J; Scarborough RM; Porter GJ;				
DR WPI; 90-007453/01.				
DR N-PSDB; Q02845.				
PT New natriuretic and vasodilator peptides - obid, using cDNA sequence				
PT encoding porcine brain natriuretic peptide and related human canine genes				
PS Example 1, Fig.1, GTPP, English.				
CC Sequences derived from porcine brain natriuretic gene can be used in part				
CC as probes to isolate similar genes from different species. Although human				
CC natriuretic related peptides (NRP) could not be isolated directly, canine				
CC NRPs could be, and these could then be used as probes to their human				
CC equivalents				
CC Sequence 131 AA;				
Query Match	48.5%; Score 334.5; DB 1; Length 131;			
Best Local Similarity	53.0%; Pred. No. 7.4e-27;			
Matches 71; Conservative 20; Mismatches 40; Indels 3; Gaps 2				
Query 1	MDPQTAPSRALLLLFLHLAFGRSHPLGSPGSASDLETSLGQRNHLGKLSLAYE	60		
DB 1	MGPRAALRR-VLLLFLLHLLLGCSHPLGSGGLASEL-PEIQGLDLRLRRVSELQAE	57		
Query 61	qtsleplqesprptvkwksrevategltghrkmvlytlraprpskmvgsgcfcgrkmdt	120		

[illegible][illegible]

PR 19-JAN-1989; US-299880.
PA (CALB) Calif Biotech Inc.
PI Sellhammer JJ, Lewicki J, Scarbrough RM, Porter GU;
DR WPI; 90-007453/01.
NR N-PDB; 002852.
PT New natriuretic and vasodilator peptides - obtd. using cDNA sequence
encoding porcine brain natriuretic peptide and related human canine genes
PS Example 4; Fig.3; 61pp. English.
CC Although human natriuretic related peptides (NRP) could not be isolated
CC directly, canine NRPs could be, and these could then be used as probes to
CC their human equivalents.
CC See also Q02845.
SQ Sequence 131 AA;

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Query Match          42.0%; Score 289.5; DB 1; Length 131;
Best Local Similarity 50.7%; Pred. No. 2.7e-22;
Matches 69; Conservative 13; Mismatches 47; Indels 7; Gaps 3

OY 1 mdpgtapsrallllflhlafigrshpyspsasdlstsglqegrnhlgkiselqve 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MEPCALPRALLLLFLHLSPGLGRPHPLGRGSPAS--EASASASELGRKQAVSELQAE 58
OY 61 qtsleppesrprtyvwksrev--ategirghkmvlytlirpsrkmgvsgccfgrkmd 118
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 59 QIALPPLRSHSPA--EAPFAGTGRPGVLAPHDSEVLQALRRLRSPKMKHKGSCGFRRLD 115
OY 119 rissssglgckvlyrh 134
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 116 RIGSLSGLCNVLRKY 131

RESULT 7
ID R62682
AC R62682; standard; Protein; 122 AA.
DT 14-JUL-1995 (first entry)
DE Hamster brain natriuretic peptide (BNP).
KW Brain natriuretic peptide; detection; vaccines.
OS Cricetus griseus.
FH Key location/Qualifiers
FT disulfide_bond 100..116
FT peptide 1..26
FT /label= sig_peptide
PN J06279496-A.
PD 04-OCT-1994.
PF 25-MAR-1993; 067113.
PR 25-MAR-1993; JP-067113.
PA (SHIO ) SHIONOGI & CO LTD.
DR WPI; 94-354771/44.
DR N-PSDB; Q73026.
PT Hamster brain derived natriuretic peptide(s) - useful for the
PT detection of BNP's, and in vaccine production
PS Claim 1; Page 5; 6pp; Japanese.
CC Q73026 encodes R62682 hamster brain natriuretic peptide (BNP).
CC R62682 can be used for the detection and determination of BNP,
CC which is useful for various reagents and medicines.
CC Sequence 122 AA;

Query Match          28.3%; Score 195; DB 1; Length 122;
Best Local Similarity 35.5%; Pred. No. 8.9e-13;
Matches 50; Conservative 23; Mismatches 42; Indels 26; Gaps 4;

OY 1 mdpgtapsrallllflhlafigrshpyspsasdlstsglqegrnhlgkiselqve 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MDLRVLRVALLFLFLFYLSPGSHSHPLGSPSOSPE-----QSKM----- 42
OY 61 qtsleppesrprtyvwksrevat-----egirghkmvlytlirpsrkmgvsgccf 113
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 42 QTLDLRLRKENAVAKGGLLKDQDVTITAPLQSTIGSQDSTIHVQLKLRNKKHNSGCF 101
OY 114 grkmdrlssssglgckvlyrh 134

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PR 10-SEP-1991: JP-230597.
 PA (DAICHI) DAICHI KAGAKU YAKUHIIN KK.
 PA (DAICHI) DAICHI PHARM CO LTD.
 DR WPI: 93-130645/16.
 PT Prepn. of physiologically active peptide without aspartic acid-proline sequence - comprises gene recombination with cell transformation by specified expression vector
 PS Claim 3: Page 6; 17pp; Japanese.
 CC This sequence represents a recombinant human brain natriuretic peptide (hBNP). This protein was encoded by the fragments of plasmids given in Q4110-04 which encode fusion peptides of murine or rat interleukin 1 (IL-1) fused to hBNP. Fusion genes of this kind can be used to express recombinant BNP which lacks the Asp-Pro N-terminal bond. The Asp residue may be replaced by Ser or may be absent.
 CC Sequence 32 AA:

Query Match 24.5%; Score 169; DB 1; Length 32;
 Best Local Similarity 100.0%; Pred. No. 7.3e-11;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 103 spkmvgsccfgrkmdrissssglgckvllrrh 134
 1 SPKMVGSCGFRKMDRISSSSGLGCKVLLRRH 32

RESULT 12
 ID R40861 standard; Protein; 32 AA.
 AC R40861;
 DT 14-MAR-1994 (first entry)
 DE BNP, brain natriuretic peptide; transformation; expression;
 KW BNP; brain natriuretic peptide; transformation; expression;
 OS Homo sapiens.
 PN J05207891-A.
 PD 20-AUG-1993.
 PF 08-MAR-1991: 043641.
 PR 08-MAR-1991: JP-043641.
 PA (SHIO) SHIONOGI & CO LTD.
 DR WPI: 93-297469/38.
 DR N-PSDB; 047829.
 PT Brain natriuretic peptide prepn. - by forming fused peptide congl. desired sequence, cleaving with restriction enzyme and collecting desired peptide
 PS Discloure; Page 8; 11pp; Japanese.
 CC The prepn. of BNP comprises: (a) obtaining a fused protein of formula X-Glu-BNP, where X is a leader sequence of 70-170 amino acids (R45761); (b) cleaving the fused protein with a restriction enzyme that can cleave between Glu and BNP.
 CC (c) collecting BNP.
 CC The BNP sequence is shown in (Q47829) and the Glu-BNP sequence is given in (Q47831).
 CC Sequence 32 AA:

Query Match 24.5%; Score 169; DB 1; Length 32;
 Best Local Similarity 100.0%; Pred. No. 7.3e-11;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 103 spkmvgsccfgrkmdrissssglgckvllrrh 134
 1 SPKMVGSCGFRKMDRISSSSGLGCKVLLRRH 32

RESULT 13
 ID W70090 standard; peptide; 32 AA.
 AC W70090;
 DT 28-OCT-1998 (first entry)
 DE Brain natriuretic peptide (BNP) 1.
 KW BNP; brain natriuretic peptide; cardiac hypertrophy; chronic heart failure; ischaemic cardiac disease; arrhythmia;

KW CGMP: pulmonary blood circulation; haemodynamic property.
 OS Unidentified.
 PN W09634636-A1.
 PD 13-AUG-1998.
 PF 05-FEB-1998; J00483.
 PR 05-FEB-1997; JP-022594.
 PA (SUNR) SUNTORY LTD.
 PI Furiya M, Hidaka T, Inomata N, Yamaki A;
 DR WPI: 98-446949/38.
 PT Drug composition comprises natriuretic peptide(s) - for safe treatment of cardiac hypertrophy associated diseases and chronic heart failure
 PS Examples: Page 23; 35pp; Japanese.
 CC This represents a brain natriuretic peptide (BNP) sequence. The invention provides a composition for treating cardiac diseases associated with cardiac hypertrophy. The composition comprises an active ingredient capable of binding to the peptide receptor of GC-A and promoting production of cGMP. The drug composition may be used clinically to treat cardiac diseases caused by cardiac hypertrophy, including chronic heart failure, ischaemic cardiac diseases and arrhythmia. The active substance can bind to the natriuretic peptide receptor of GC-A and promote production of cGMP, effectively preventing cardiac hypertrophy and leading to improvement of the pulmonary blood circulation. The substance does not affect haemodynamic properties, blood pressure, heart beat and urine volume.
 CC Sequence 32 AA:

Query Match 24.5%; Score 169; DB 1; Length 32;
 Best Local Similarity 100.0%; Pred. No. 7.3e-11;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 103 spkmvgsccfgrkmdrissssglgckvllrrh 134
 1 SPKMVGSCGFRKMDRISSSSGLGCKVLLRRH 32

RESULT 14
 ID W67040 standard; peptide; 32 AA.
 AC W67040;
 DT 15-DEC-1998 (first entry)
 DE Brain natriuretic peptide (BNP).
 KW atrial natriuretic peptide; brain natriuretic peptide; ANP; BNP; renal disorder.
 OS Mammalia.
 FH Key
 FT Location/Qualifiers
 FT 2..32 "this fragment having a lipophilic group attached to it is claimed in Claim 33"
 FT 3..32 "this fragment having a lipophilic group attached to it is claimed in Claim 33"
 FT 4..32 "this fragment having a lipophilic group attached to it is claimed in Claim 33"
 FT 5..32 "this fragment having a lipophilic group attached to it is claimed in Claim 33"
 FT 6..32 "this fragment having a lipophilic group attached to it is claimed in Claim 33"
 FT 7..32 "this fragment having a lipophilic group attached to it is claimed in Claim 33"
 FT 8..32 "this fragment having a lipophilic group attached to it is claimed in Claim 33"
 FT 9..32 "this fragment having a lipophilic group attached to it is claimed in Claim 33"
 FT 10..32 "this fragment having a lipophilic group attached to it is claimed in Claim 33"
 FT Disulfide_bond 10..32

Search completed: April 27, 2000, 18:29:23
 Job time: 2793 sec

FT K09845329-A1. /label= disulphide_bond
 PN 15-OCT-1998.
 PD 06-APR-1998; DK0142.
 PR 04-APR-1997; US-043400.
 PA (NOVO) NOVO-NORDISK AS.
 PI Hunsfeldt PO, Knudsen LB, Madsen K;
 DR WPI: 98-557474/47
 PT Lipophilic derivatives of atrial and brain natriuretic peptides -
 PT notably as amides, prolong activity, use in hypertension, congestive
 PT heart failure, renal disorders, oedema, and hepatic cirrhosis.
 PS Claim 32: Pages 1-2; 23pp; English.
 CC The invention relates to natriuretic derivatives, containing a lipophilic
 CC substituent attached to any one amino acid residue. Also new are
 CC natriuretic derivatives as above, but with two attached lipophilic
 CC substituents. Atrial natriuretic (ANP) and brain natriuretic (BNP)
 CC peptides are already used in treatment of various diseases, and it is
 CC believed that the lipophilic derivatives will have similar uses. These
 CC diseases include hypertension, congestive heart failure, oedema, renal
 CC disorders, and hepatic cirrhosis. The lipophilic group protects the
 CC peptide from metabolic breakdown, increasing the duration of action. The
 CC present sequence represents BNP.
 CC Sequence 32 AA;

Query Match 24.5%; Score 169; DB 1; Length 32;
 Best Local Similarity 100.0%; Pred. No. 7.3e-11;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 103 spkmvgsqcfgrkmdrissssglgckvllrrh 134
 ||||||||||||||||||||||||||||
 Db 1 SPKMVGSGCFGRKMDRISSSSGLGCKVLRH 32

RESULT 15
 R35490
 ID R35490 standard; peptide; 33 AA.
 AC R35490;
 DT 26-AUG-1993 (first entry)
 DE Tyr-hBNP.
 KW Human; brain natriuretic peptide; specificity: monoclonal; antibody;
 KW MAb; hBNP; Hydrindoma; BC203; label; detection; hBNP/MAB complex.
 OS Synthetic.
 PN EP-542255-A.
 PD 19-MAY-1993.
 PC 12-NOV-1992; 119353.
 PC 14-NOV-1991; JP-326961.
 PI (SHIO) SHIONOGI SEIRYAKU KK.
 PI Igano K, Inouye K, Kono M, Tsuji T, Yamauchi A;
 DR WPI: 93-160757/20.
 PT Monoclonal antibody recognising the C-terminus of hBNP - for
 PT determining hBNP levels in blood plasma by immunoassay; useful
 PT for diagnosing hypertension
 PS Disclosure; Page 9; 13pp; English.
 CC This sequence represents Tyr-hBNP (human brain natriuretic peptide).
 CC This peptide was used in determining the specificity of a monoclonal
 CC antibody (MAb) which recognises the C-terminal of hBNP. The MAb is
 CC produced by hydrindoma BC203 (PERM BP-3515). The Tyr residue had to
 CC be added to the N-terminal of the hBNP as no other Tyr appears
 CC within the molecule and this residue was used to carry a label to
 CC allow detection of the hBNP/MAB complex.
 CC Sequence 33 AA;

Query Match 24.5%; Score 169; DB 1; Length 33;
 Best Local Similarity 100.0%; Pred. No. 7.6e-11;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 103 spkmvgsqcfgrkmdrissssglgckvllrrh 134
 ||||||||||||||||||||||||||||
 Db 2 SPKMVGSGCFGRKMDRISSSSGLGCKVLRH 33

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 27, 2000, 18:26:25 ; Search time 14.62 Seconds

(without alignments)
432.332 Million cell updates/sec

Title: PEPI

Perfect score: 690
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 142080 seqs, 47169319 residues

Total number of hits satisfying chosen parameters: 142080

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :
1: PIR_62:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	690	100.0	134	1 AMWHB	natriuretic peptid
2	334.5	48.5	131	2 A33873	brain natriuretic
3	328.5	47.6	131	2 A33876	brain natriuretic
4	204.5	35.7	103	2 A41403	aldosterone secret
5	204.5	29.6	105	2 B36736	brain natriuretic
6	171.5	24.9	121	1 A30162	brain natriuretic
7	165.5	24.0	121	2 I49548	brain natriuretic
8	164.5	23.8	121	2 A49144	type-B natriuretic
9	137	19.9	140	1 S14320	alpha-atrial natrl
10	118	17.1	149	1 AMWB	atrial natriuretic
11	118	17.1	152	1 AMBO	atrial natriuretic
12	113	16.4	151	1 AMWU	natriuretic peptid
13	113	16.4	153	2 S14873	atrial natriuretic
14	109.5	15.9	150	1 S13107	atrial natriuretic
15	106	15.4	27	2 JC1081	brain natriuretic
16	105.5	15.3	153	1 AMRB	atrial natriuretic
17	104	15.1	145	1 JC0947	atrial natriuretic
18	100	14.5	152	1 AMMS	atrial natriuretic
19	97	14.1	152	1 AMWR	atrial natriuretic
20	90.5	13.1	115	1 S15822	natriuretic peptid
21	88	12.8	126	1 A36155	natriuretic peptid
22	87.5	12.7	126	2 S12988	brain natriuretic
23	87	12.6	37	2 S71382	lebetin 2 isoform
24	86.5	12.5	126	1 AMHUC	natriuretic peptid
25	86.5	12.5	126	1 A61244	natriuretic peptid
26	85.5	12.4	126	2 A55688	natriuretic peptid
27	85.5	12.4	126	2 A55688	natriuretic peptid
28	84	12.2	129	1 A54119	C-type natriuretic
29	82.5	12.0	128	2 S14872	atrial natriuretic
30	82	11.9	161	4 I55480	hypothetical natrl

31	81.5	11.8	118	2 B54119	C-type natriuretic
32	81.5	11.7	1677	2 T14267	Xin protein, stage
33	81	11.7	30	2 S01657	atrial natriuretic
34	80.5	11.7	1319	1 C43735	bcsd protein - Ace
35	78	11.3	22	2 A35418	brain natriuretic
36	77	11.2	36	2 S15821	ventricular natru
37	74.5	10.8	1065	2 T13230	dachshund isoform
38	74.5	10.8	1072	2 T13228	dachshund protein
39	74.5	10.8	1072	2 T13232	dachshund protein
40	74.5	10.8	1074	2 T13229	dachshund protein
41	74.5	10.8	1081	2 T13231	C-type natriuretic
42	74	10.7	22	2 A36399	atrial natriuretic
43	74	10.7	27	2 A33431	serine proteinase
44	74	10.7	786	1 A47547	natriuretic peptid
45	72	10.4	22	2 J10581	

ALIGNMENTS

RESULT 1

AMWHB
natriuretic peptide B precursor - human
N:Alternate names: brain natriuretic factor-32 (BNF-32); brain natriuretic protein pr
N:Contains: brain alpha natriuretic peptide; brain gamma natriuretic factor
C:Species: Homo sapiens (man)
C:date: 07-Sep-1990 #sequence, revision 02-Dec-1994 #text_change 18-Jun-1999
C:Accession: A36736; A30163; A34143; A34661; B34661
R:Seilhamer, J. J.; Arfsten, A.; Miller, J. A.; Lundquist, P.; Scarborough, R. M.; Lewic
Biochem. Biophys. Res. Commun. 165, 650-658, 1989
A:Title: Human and canine gene homologs of porcine brain natriuretic peptide.
A:Reference number: A36736; MUID:90086474
A:Accession: A36736
A:Molecule type: DNA
A:Residues: 1-134 <SEI>
A:Cross-references: GB:M31776; NID:9179514; PID:AAA35603.1; PID:9179515
R:Sudoh, T.; Maekawa, K.; Kojima, M.; Minamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 159, 1427-1434, 1989
A:Title: Cloning and sequence analysis of cDNA encoding a precursor for human brain n
A:Reference number: A30163; MUID:89193743
A:Accession: A30163
A:Molecule type: mRNA
A:Residues: 1-134 <SD>
A:Cross-references: GB:M31776; NID:9179514; PID:AAA35603.1; PID:9179515
R:Ramakrishna, Y.; Nakao, K.; Mukoyama, M.; Saito, Y.; Ogawa, Y.; Shiono, S.; Inouye,
FEBS Lett. 259, 341-345, 1990
A:Title: Isolation and sequence determination of human brain natriuretic peptide in h
A:Reference number: A34143; MUID:90092577
A:Accession: A34143
A:Molecule type: protein
A:Residues: 103-134 <KAM>
R:Hino, J.; Tateyama, H.; Minamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 167, 693-700, 1990
A:Title: Isolation and identification of human brain natriuretic peptides in cardiac
A:Reference number: A30161; MUID:90211249
A:Accession: A34661
A:Molecule type: protein
A:Residues: 27-58 <HIN>
A:Accession: B34661
A:Molecule type: protein
A:Residues: 103-134 <H12>
C:Genetics:
A:Gene: GDB:NPPR
A:Cross-references: GDB:127884; OMIM:600295
A:Map position: 1p36-1p36
A:introns: 44/3; 130/1
C:Superfamily: natriuretic peptide A precursor
C:Keywords: brain; diuretic; hormone; natriuretic; osmoregulation
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-134/Product: brain gamma natriuretic factor #status experimental <GNF>
F:103-134/Product: brain alpha natriuretic peptide #status experimental <ANF>
F:112-128/Disulfide bonds: #status predicted

RESULT

5

B36736
brain natriuretic peptide - dog

C:Species: Canis lupus familiaris (dog)
C>Date: 19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change 09-Dec-1994
C:Accession: B36736
R:Seilheimer, J.J.; Artstien, A.; Miller, J.A.; Lundquist, P.; Scarborough, R.M.; Lewicki,
Biochem. Biophys. Res. Commun. 165, 650-658, 1989
A>Title: Human and canine gene homologs of porcine brain natriuretic peptide.
A:Reference number: A36736; MUID:90088474
A:Accession: B36736
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-105 <SEI>
A:Cross-references: GB:M31777
C:Superfamily: natriuretic peptide A precursor

Query Match 29.6%; Score 204.5; DB 2; Length 105;
Best Local Similarity 45.5%; Pred. No. 6.1e-13;
Matches 50; Conservative 11; Mismatches 42; Indels 7; Gaps 3;

Oy 27 hplgpgsasdlqetsglqegrnhlgkislqlveqtslepiqesprptcgvksrev--at 84
||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 HPLGGRSPASG-AEASELLGLRLKDAVSELQAEGLALEPILHRSHSPA---EAPAGGTP 55
||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Oy 85 egfgrhkrmvlytlraprskmvgsgcgfrkmrdissssglgcgvllrrh 134
||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 56 RGVLAPHDSVLAALRLRS PKMKHKS GCGFRRLDRIGSLSGLCNVLRKY 105
||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT

6

A30162
brain natriuretic factor precursor - rat

N:Alternate names: brain natriuretic peptide; cardiac natriuretic factor; iso-atrial natu
N:Contains: brain natriuretic factor BNP-45
C:Species: Rattus norvegicus (Norway rat)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A30162; A33691; A54893; A32918; A32819; A33253; A60735; I57704; A33252
R:Koijima, M.; Minamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 159, 1420-1426, 1989
A>Title: Cloning and sequence analysis of cDNA encoding a precursor for rat brain natru
A:Reference number: A30162; MUID:89193742
A:Accession: A30162
A:Molecule type: mRNA
A:Residues: 1-121 <KOJ>
A:Cross-references: GB:M5297; NID:g602483; PIDN:AAA57269.1; PID:g602484
R:Foy, R.N.; Flynn, T.G.
Biochem. Biophys. Res. Commun. 171, 416-423, 1990
A>Title: Organization of the gene for Iso-rANP, a rat B-type natriuretic peptide.
A:Reference number: A33691; MUID:90365739
A:Accession: A33691
A:Molecule type: DNA
A:Residues: 1-14,'V','16'-121 <ROY>
A:Cross-references: GB:M60731; NID:g204985; PIDN:AAAA1456.1; PID:g204986
A>Note: The authors translated the codon GTT for residue 15 as Leu
R:Thierauf, D.J.; Hanford, D.S.; Glombotski, C.C.
J. Biol. Chem. 269, 17772-17775, 1994
A>Title: Regulation of rat brain natriuretic peptide transcription. A potential role for
A:Reference number: A54893; MUID:94299479
A:Accession: A54893
A:Molecule type: DNA
A:Residues: 1-19 <THD>
A:Cross-references: GB:U02972; NID:g458021; PIDN:AA21648.1; PID:g458022
R:Ashuraya, M.; Hiro, Y.; Minamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 163, 226-232, 1989
A>Title: Isolation and identification of rat brain natriuretic peptides in cardiac atriu
A:Reference number: A32918; MUID:89374230

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A:Accession: A32918
A:Molecule type: protein
A:Residues: 27-121 <ABU>
R:Kambayashi, Y.; Nakao, K.; Itoh, H.; Hosoda, K.; Salto, Y.; Yamada, T.; Mukoyama, M.; Imura, H.
Biochem. Biophys. Res. Commun. 163, 233-240, 1989
A:Title: Isolation and sequence determination of rat cardiac natriuretic peptide.
A:Reference number: A32919; MUID:89374231
A:Accession: A32919
A:Molecule type: protein
A:Residues: 77-121 <RAM>
R:Flynn, T.G.; Brar, A.; Tremblay, L.; Sarda, I.; Lyons, C.; Jennings, D.B.
Biochem. Biophys. Res. Commun. 161, 830-837, 1989
A:Title: Isolation and characterization of iso-rANP, a new natriuretic peptide from r
A:Reference number: A33253; MUID:89286593
A:Accession: A33253
A:Molecule type: protein
A:Residues: 77-119, '0', 121 <Flx>
R:Nakao, K.; Itoh, H.; Kambayashi, Y.; Hosoda, K.; Salto, Y.; Yamada, T.; Mukoyama, M.
Hypertension 15, 774-778, 1990
A:Title: Rat brain natriuretic peptide. Isolation from rat heart and tissue distribut
A:Reference number: A60735; MUID:90277148
A:Accession: A60735
A:Molecule type: protein
A:Residues: 77-121 <NAK>
R:Dagnino, L.; Drouin, J.; Nemer, M.
Mol. Endocrinol. 5, 1292-1300, 1991
A:Title: Differential expression of natriuretic peptide genes in cardiac and extrac
A:Reference number: 157704; MUID:92123224
A:Accession: 157704
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-121 <RES>
A:Cross-references: GB:M60266; MID:g204983; PIDN:AAA41455.1; PID:g204984
C:Genetics:
A:Introns: 42/3; 117/1
C:Superfamily: natriuretic peptide A precursor
C:Keywords: cardiac muscle; heart
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-121/Product: brain natriuretic factor #status experimental <MAT1>
F:77-121/Product: brain natriuretic factor BNP-45 #status experimental <MAT2>

Query Match 24.98; Score 171.5; DB 1; Length 121;
Best Local Similarity 37.14; Pred. No. 1.1e-09;
Matches 49; Conservative 18; Mismatches 52; Indels 13; Gaps 4;

QY 1 mdgptasralllllflhlaflgrshpnlpggsasdsletsgldeqrnhlgklselqve 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MDQKVLVPMILLLFLPLSLPLGSHPLGSPSOSP--EOSTMOKLELLEKSEEMAQR 58

QY 61 qtslelpdesprptgvvsksevatelgrhkmvlytlraprpskmvqsgcfrgmndri 120
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 59 Q-----LSKDGPR-----KELLRKVLRSQDSARIGERL-RNSKMAHSSSCFQGXDR 107

QY 121 ssssglgckvrlr 132
|||:|||||:
Db 108 GAVSRLGCDGLR 119

RESULT 7
149548
brain natriuretic peptide - mouse.
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C:Accession: I49548
R:Ogawa, Y.; Itoh, H.; Tamura, N.; Suga, S.; Yoshimasa, T.; Uehira, M.; Matsuda, S.;
J. Clin. Invest. 93, 1911-1921, 1994
A:Title: Molecular cloning of the complementary DNA and gene that encode mouse brain
A:Reference number: I49548; MUID:94237953
A:Accession: I49548
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

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RESULT 11

AMBO

atrial natriuretic peptide precursor - bovine

N/Alternate names: ANP; atrial natriuretic polypeptide

C/Species: Bos primigenius taurus (cattle)

C/Date: 30-Jun-1989 #sequence-revision 30-Jun-1989 #text-change 18-Jun-1999

A/Accession: A010124; A93049; A24247; A26090

R/Vlasuk, G.P.; Miller, J.; Bensen, G.H.; Lewicki, J.A.

Biochem. Biophys. Res. Commun. 136, 396-403, 1986

A/Title: Structure and analysis of the bovine atrial natriuretic peptide precursor gene.

A/Reference number: A90124; MUID:86215205

A/Accession: A90124

A/Molecule type: DNA

A/Residues: 1-152 <VNA>

A/Cross-references: GB:M3145; NID:g162665; PIDN:AAA30375.1; PID:g162666

R/Ono, H.; McNICOLL, N.; Lazure, C.; Seidah, N.; Chretien, M.; Cantlin, M.; De Lean, A.

Life Sci. 38, 1309-1315, 1986

A/Title: Purification and sequence determination of bovine atrial natriuretic factor.

A/Reference number: A93049; MUID:86173941

A/Accession: A93049

A/Molecule type: Protein

A/Residues: 123-150 <ONG>

C/Genetics:

A/Introns: 40/3; 149/3

C/Superfamily: natriuretic peptide A precursor

C/Keywords: atrium; diuretic; hormone; natriuretic; osmoregulation

F:1-24/Domain: signal sequence #status predicted <SIG>

F:123-150/Product: gamma atrial natriuretic factor #status predicted <ANP>

F:123-150/Product: alpha atrial natriuretic peptide #status experimental <ANP>

F:129-145/Disulfide Bonds: #status predicted

Query Match 17.1%; Score 118; DB 1; Length 152;

Best Local Similarity 29.6%; Pred. No. 0.00019;

Matches 47; Conservative 20; Mismatches 46; Indels 46; Gaps 8;

Db 8 stralllllflhlafl-19grshp19pspsasdlsglqgrhlgk1-----se1q 58

Db 3 SSAIVTSFLFLAFQLPQGTGANPYGVSNSMDLDFKULDRLEKMLEDEANVPSQVL 62

Oy 59 vevts-----leplqesp-----rptgv-----ksrevateglrghrkmvlyt- 98

Db 63 SEQNEAGAPLSPLEMPWMEVNPAPQREGVGLGKGPWESSD-----RSALTKSK 113

Oy 98 ----lraprpkvmvgsgcfcgfkmdrisssglqckvlr 132

Db 114 LRAULTAPRS---LRRSSCFGGKMDRIGASGLGCSNFR 149

RESULT 12

AMHU

natriuretic peptide A precursor - human

N/Alternate names: ANP; atrial natriuretic factor; atrial natriuretic protein; prepronat

C/Contains: atrial alpha natriuretic peptide (ANP); cardiolipatin (atrial gamma natriure

C/Species: Homo sapiens (man)

C/Date: 15-Nov-1984 #sequence-revision 15-Nov-1984 #text-change 18-Jun-1999

A/Accession: A22693; B22693; A01424; B29370; A32733; I58054; S14097; I39455; I39459; I39

R/Nemer, M.; Chamberland, M.; Strots, D.; Argentin, S.; Drouin, J.; Dixon, R.A.F.; Zivlin

Nature 312, 654-656, 1984

A/Title: Gene structure of human cardiac hormone precursor, pronatriodilatin.

A/Reference number: A22693; MUID:85061626

A/Accession: A22693

A/Molecule type: DNA

A/Residues: 1-151 <NEM>

A/Cross-references: GB:X01470; NID:g28687; PIDN:CAA25659.1; PID:g823625

A/Accession: B22693

A/Molecule type: DNA

A/Residues: 1-151, 'RR' <NE2>

A/Note: allelic variant with UGA termination codon replaced by CGA arginine codon

R/Oikawa, S.; Imai, M.; Denc, A.; Tanaka, S.; Noguchi, T.; Nakazato, H.; Kangawa, K.; Fu

Nature 309, 724-726, 1984

A/Title: Cloning and sequence analysis of cDNA encoding a precursor for human atrial nat

A/Reference number: A01424; MUID:84219799

A/Accession: A01424

A/Molecule type: mRNA

A/Residues: 1-151 <OIR>

A/Cross-references: GB:K02043; NID:g178629; PIDN:AB59379.1; PID:g178630

R/Setdman, C.E.; Bloch, K.D.; Kiehl, R.A.; Smith, J.A.; Setdman, J.G.

Science 226, 1206-1209, 1984

A/Title: Nucleotide sequences of the human and mouse atrial natriuretic factor genes.

A/Reference number: A29370; MUID:85065766

A/Accession: B29370

A/Molecule type: DNA

A/Residues: 1-64, 'D', 66-151 <SEI>

A/Cross-references: GB:K02043

A/Title: Purification and complete amino acid sequence of alpha-human atrial natriure

A/Reference number: A2733; MUID:84128019

A/Accession: A2733

A/Molecule type: Protein

A/Residues: 124-151 <KAN>

R/Nakayama, K.; Ohkubo, H.; Hirose, T.; Inayama, S.; Nakanishi, S.

Nature 310, 699-701, 1984

A/Title: mRNA sequence for human cardiolipatin-atrial natriuretic factor precursor an

A/Reference number: I58054; MUID:84295577

A/Accession: I58054

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-151 <RES>

A/Cross-references: GB:M30262; NID:g180181; PIDN:AAA35669.1; PID:g180182

R/Vansteede, Y.; Michel, A.; Deschodt-Lanckman, M.

Eur. J. Biochem. 196, 281-286, 1991

A/Title: Hydrolysis of intact and Cys-Phe-cleaved human atrial natriuretic peptide in

A/Reference number: S14097; MUID:91176998

A/Accession: S14097

A/Molecule type: Protein

A/Residues: 124-151 <VAN>

A/Note: natural and synthetic peptide subjected to kallikrein proteolysis

R/Vansteede, Y.; Michel, A.; Deschodt-Lanckman, M.

Proc. Natl. Acad. Sci. U.S.A. 81, 6325-6329, 1984

A/Title: Molecular cloning and characterization of DNA sequences encoding rat and hum

A/Reference number: I39458; MUID:85038509

A/Accession: I39458

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 119-151, 'RR' <RE2>

A/Cross-references: GB:K02044; NID:g178631; PIDN:AAA51730.1; PID:g178632

R/Maki, M.; Parmentier, M.; Inagami, T.

Biochem. Biophys. Res. Commun. 125, 797-802, 1984

A/Title: Cloning of genomic DNA for human atrial natriuretic factor.

A/Reference number: I39459; MUID:85069683

A/Accession: I39459

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-64, 'D', 66-151 <RE4>

A/Cross-references: GB:M54951; NID:g178636; PIDN:AAA35529.1; PID:g178638

R/Greeneberg, B.D.; Bensen, G.H.; Sellhammer, J.J.; Lewicki, J.A.; Fliddes, J.C.

Nature 312, 656-658, 1984

A/Title: Nucleotide sequence of the gene encoding human atrial natriuretic factor pre

A/Reference number: I37167; MUID:85061627

A/Accession: I37167

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 26-151 <RE5>

A/Cross-references: EMBL:X01471; NID:g28690

C/Comment: Cardiolipatin is a vasoconstrictor but not a diuretic or natriuretic.

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 27, 2000, 18:29:24 ; Search time 8.53 Seconds

(without alignments)
469.135 Million cell updates/sec

Title: PEPI
Perfect score: 690
Sequence: 1 mdptapsralllllflhla.....rkmdrlsssgslgckvlrrh 134

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 82229 seqs, 29864866 residues

al number of hits satisfying chosen parameters: 82229

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SwissProt_38.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	690	100.0	134	1 ANFB_HUMAN	P18660 homo sapien
2	334.5	48.5	131	1 ANFB_PIG	P07634 sus scrofa
3	296	42.9	140	1 ANFB_CANFA	P16859 canis famill
4	246.5	35.7	103	1 ANFB_BOVIN	P13204 bos taurus
5	171.5	24.9	121	1 ANFB_RAT	P13205 rattus norv
6	165.5	24.0	121	1 ANFB_MOUSE	P40753 mus musculu
7	137	19.9	140	1 ANFB_CHICK	P16908 gallus gall
8	118	17.1	149	1 ANFB_BOVIN	P07499 canis famill
9	113	16.4	152	1 ANFB_HORSE	P27104 equus caball
10	113	16.4	153	1 ANFB_HUMAN	P01160 homo sapien
11	113	16.4	153	1 ANFB_HUMAN	P01160 homo sapien
12	109.5	15.9	150	1 ANFB_PIG	P21259 sus scrofa
13	105.5	15.3	153	1 ANFB_RABIT	P07500 oryctolagus
14	104	15.1	145	1 ANFB_RANCA	P18909 rana catesb
15	100	14.5	152	1 ANFB_MOUSE	P01125 mus musculu
16	97	14.1	152	1 ANFB_RAT	P01161 rattus norv
17	92.5	13.4	126	1 ANFC_BOVIN	P55206 bos taurus
18	92.5	13.4	126	1 ANFC_SHEEP	P56283 ovis aries
19	90.5	13.1	115	1 ANFC_SCYCA	P22259 scyliorhinu
20	88	12.7	126	1 ANFC_PIG	P18104 sus scrofa
21	87.5	12.5	126	1 ANFC_RAT	P51207 rattus norv
22	86.5	12.5	126	1 ANFC_HUMAN	P23582 homo sapien
23	86.5	12.5	135	1 ANFC_SQUAC	P41319 squalus aca
24	85.5	12.4	115	1 ANFC_TRISC	P55208 triakis scy
25	85.5	12.4	126	1 ANFC_MOUSE	P06183 mus musculu
26	84	12.2	129	1 ANFC_RANCA	P20968 rana catesb
27	83.5	12.1	131	1 ANFC_ANGJA	P18145 anguilla ja
28	82.5	12.0	128	1 ANFC_CAVPO	P27596 cavla porce
29	81.5	11.8	118	1 ANFD_RANCA	P40756 rana ridibu
30	81	11.7	30	1 ANFB_RANRI	P09196 rana ridibu
31	80.5	11.7	1319	1 ACSC_ACERY	P10450 acetobacter
32	77	10.9	36	1 ANFB_ANGJA	P26442 anguilla ja
33	75.5	10.9	780	1 OBP_HSV62	P52452 herpes simp
34	74.5	10.8	780	1 OBP_HSV62	P52378 herpes simp

ALIGNMENTS

RESULT	1	ANFB_HUMAN	STANDARD:	PRT:	134 AA.
AC	01-AUG-1990 (Rel. 15, Created)				
DT	01-AUG-1990 (Rel. 15, Last sequence update)				
DT	15-DEC-1998 (Rel. 37, Last annotation update)				
DE	BRAIN NATRIURETIC PEPTIDE PRECURSOR (BNP).				
GN	NPPH.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;				
OC	Eukaryota; Primates; Catarrhini; Hominoidea; Homo.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE: 90088474.				
RA	SEITZHAMER J.J., ARFSTEN A., MILLER J.A., LUNDQUIST P.,				
RA	SCARBOROUGH R.M., LEWICKI J.A., PORTER J.G.;				
RT	"Human and canine gene homologs of porcine brain natriuretic peptide.";				
RT	Biochem. Biophys. Res. Commun. 159:1427-1434(1989).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RA	ERRINGTON H.;				
RL	Submitted (May-1998) to the EMBL/GenBank/DBJ databases.				
RN	[4]				
RP	SEQUENCE OF 27-58 AND 103-134.				
RX	MEDLINE: 90211249.				
RA	HINO J., TATEYAMA H., MINAMINO N., KANGAWA K., MATSUO H.;				
RT	"Isolation and sequence determination of human brain natriuretic peptide in human atrium.";				
RT	Biochem. Biophys. Res. Commun. 167:693-700(1990).				
RN	[5]				
RP	SEQUENCE OF 103-134.				
RX	MEDLINE: 90092577.				
RA	KABARASHI Y., NAKAO K., MUKOTYAMA M., SAITO Y., OGAWA Y., SHONO S.;				
RA	INOUE K., YOSHIDA N., IMURA H.;				
RT	"Isolation and sequence determination of human brain natriuretic peptide in human atrium.";				
RT	FEBS Lett. 259:341-345(1990).				
RL	-1- FUNCTION: VASOACTIVE ACTIVITY.				
CC	-1- TISSUE SPECIFICITY: BRAIN AND ALSO IN ATRIA, BUT AT MUCH LOWER LEVELS THAN ANP.				
CC	-1- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/)				

Db 118 GSLSGCNCVLRKY 131

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RESULT 3
ANFB_CANFA STANDARD; PRT; 140 AA.
ID ANFB_CANFA
AC P16859:
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE BRAIN NATRIURETIC PEPTIDE PRECURSOR (BNP).
GN NPPB.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Canidae; Canis.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90088474.
RA SEILHAMER J.J., ARSTEN A., MILLER J.A., LUNDQUIST P.,
RA SCARBOROUGH R.M., LEWICKI J.A., PORTER J.G.;
"Human and canine gene homologs of porcine brain natriuretic
peptide."
CC Biochem. Biophys. Res. Commun. 165:650-658(1989).
CC -1- FUNCTION: VASOACTIVE ACTIVITY.
CC -1- TISSUE SPECIFICITY: BRAIN AND ALSO IN ATRIA, BUT AT MUCH LOWER
CC LEVELS THAN ANP.
CC -1- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; M31777; AAA30832.1; -
DR PIR; B36736; B36736
DR PROSITE; P500263; NATRIURETIC_PEPTIDE; 1.
DR PFAM; PF00212; ANP; 1.
KW Vasoactive; Brain; Signal.
FT SIGNAL 1 26
FT CHAIN 27 140 POTENTIAL.
FT PEPTIDE 107 140 GAMMA-BRAIN NATRIURETIC PEPTIDE.
FT PEPTIDE 112 140 BRAIN NATRIURETIC PEPTIDE (BNP-34).
FT DISULFID 118 134 BRAIN NATRIURETIC PEPTIDE (BNP-29).
SQ SEQUENCE 140 AA; 14966 MW; DCEBC52 CRC32;

Query Match 42.9%; Score 296; DB 1; Length 140;
Best Local Similarity 50.3%; Pred. No. 8.2e-22;
Matches 72; Conservative 14; Mismatches 45; Indels 12; Gaps 4;

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DE BRAIN NATRIURETIC PEPTIDE PRECURSOR (BNP) (ALDOSTERONE SECRETION
INHIBITORY FACTOR) (ASIF).
GN NPPB.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Bovine; Bos.
RN [1]
RP SEQUENCE.
RX MEDLINE; 9011487.
RA NGUYEN T.T., LAZURE C., BABINSKI K., CHRETIEN M., DE LEAN A., ONG H.;
"Identification and primary structure of pro-aldosterone secretion
inhibitory factor from bovine adrenal chromaffin cells."
RT Mol. Endocrinol. 3:1823-1829(1989).
RN [2]
RP SEQUENCE OF 69-103.
RX MEDLINE; 89136947.
RA NGUYEN T.T., LAZURE C., BABINSKI K., CHRETIEN M., ONG H., DE LEAN A.;
"aldosterone secretion inhibitory factor: a novel neuropeptide in
bovine chromaffin cells."
RT Endocrinology 124:1591-1593(1989).
CC -1- FUNCTION: INHIBITS ALDOSTERONE SECRETION.
CC -1- TISSUE SPECIFICITY: BRAIN AND ALSO IN ATRIA, BUT AT MUCH LOWER
CC LEVELS THAN ANP.
CC -1- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
DR PIR; A41403; A41403.
DR PROSITE; P500263; NATRIURETIC_PEPTIDE; 1.
DR PFAM; PF00212; ANP; 1.
KW Vasoactive; Brain.
FT CHAIN 1 103 GAMMA-BRAIN NATRIURETIC PEPTIDE.
FT PEPTIDE 69 103 ALDOSTERONE SECRETION INHIBITORY FACTOR.
FT PEPTIDE 78 103 BRAIN NATRIURETIC PEPTIDE (BNP-26).
FT DISULFID 81 97
SQ SEQUENCE 103 AA; 11249 MW; E3823460 CRC32;

Query Match 35.7%; Score 246.5; DB 1; Length 103;
Best Local Similarity 49.1%; Pred. No. 3.2e-17;
Matches 53; Conservative 14; Mismatches 36; Indels 5; Gaps 2;

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RESULT 5
ANFB_RAT STANDARD; PRT; 121 AA.
ID ANFB_RAT
AC P13205;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE BRAIN NATRIURETIC PEPTIDE PRECURSOR (BNP) (5 KD CARDIAC NATRIURETIC
PEPTIDE) (ISO-ANP).
GN NPPB.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89193742.
RA KOJIMA M., MINAMINO N., KANGAWA K., MATSUO H.;
"Cloning and sequence analysis of cDNA encoding a precursor for rat
brain natriuretic peptide."
RT Biochem. Biophys. Res. Commun. 159:1420-1426(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90365739.

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RA ROY R.N., FLYNN T.G.;
 RT "Organization of the gene for iso-rANP, a rat B-type natriuretic
 peptide.";
 RL Biochem. Biophys. Res. Commun. 171:416-423(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 92123224.
 RA DAGNINO L., DROUIN J., NEMER M.;
 RT "Differential expression of natriuretic peptide genes in cardiac and
 extracardiac tissues.";
 RL Mol. Endocrinol. 5:1292-1300(1991).
 RN [4]
 RP SEQUENCE OF 27-121.
 RX MEDLINE; 89374230.
 RA ABRYARA M., HINO J., MINAMINO N., KANGAWA K., MATSUO H.;
 RT "Isolation and identification of rat brain natriuretic peptides in
 cardiac atrium.";
 RL Biochem. Biophys. Res. Commun. 163:226-232(1989).
 RN [5]
 RP SEQUENCE OF 77-121.
 RX TISSUE-HEART;
 RA MEDLINE; 89374231.
 RA KAMBAYASHI Y., NAKAO K., ITOH H., HOSODA K., SAITO Y., YAMADA T.,
 RA MORIOYAMA M., ARAI H., SHIRAKAMI G., SUGA S.-I., OGAWA Y.,
 RA JOUGASAKI M., MINAMINO N., KANGAWA K., MATSUO H., INOUE K., IMURA H.;
 RT "Isolation and sequence determination of rat cardiac natriuretic
 peptide.";
 RL Biochem. Biophys. Res. Commun. 163:233-240(1989).
 RN [6]
 RP SEQUENCE OF 77-121.
 RX MEDLINE; 89286593.
 RA FLYNN T.G., BRAR A., TREMBLAY L., SARDA I., LYONS C., JENNINGS D.B.;
 RT "Isolation and characterization of iso-rANP, a new natriuretic
 peptide from rat atria.";
 RL Biochem. Biophys. Res. Commun. 161:830-837(1989).
 RN [7]
 RP SEQUENCE OF 99-115.
 RX MEDLINE; 89286579.
 RA ITOH H., NAKAO K., KAMBAYASHI Y., HOSODA K., SAITO Y., YAMADA T.,
 RA MORIOYAMA M., ARAI H., SHIRAKAMI G., SUGA S.-I., YOSHIDA I., INOUE K.,
 RA IMURA H.;
 RT "Occurrence of a novel cardiac natriuretic peptide in rats.";
 RL Biochem. Biophys. Res. Commun. 161:732-739(1989).
 CC [1-] FUNCTION: VASOACTIVE ACTIVITY.
 CC [1-] TISSUE SPECIFICITY: BRAIN AND ALSO IN ATRIA, BUT AT MUCH LOWER
 LEVELS THAN ANP.
 CC [1-] SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
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 or send an email to license@isb-sib.ch).
 CC EMBL; M25297; AAA57269.1; -;
 DR EMBL; M60731; AAA41456.1; -;
 DR EMBL; M60266; AAA41455.1; -;
 DR PIR; A30162; A30162.
 DR PIR; A32918; A32918.
 DR PIR; A32919; A32919.
 DR PIR; A33252; A33252.
 DR PIR; A33253; A33253.
 DR PIR; A35691; A35691.
 DR PROSITE; PS00263; NATRIURETIC-PEPTIDE; 1.
 DR PIR; PF00212; ANP; 1.
 DR KW Vasoactive; Brain; Signal.
 FT SIGNAL 1 26
 FT PEPTIDE 27 121 GAMMA-BRAIN NATRIURETIC PEPTIDE.
 FT PEPTIDE 77 121 BRAIN NATRIURETIC PEPTIDE (5 KD CARDIAC
 FT DISULFID 99 115 NATRIURETIC PEPTIDE) (BNP-45).

FT CONFLICT 15 15 L -> V (IN REF. 2).
 FT CONFLICT 120 120 L -> Q (IN REF. 6).
 SQ SEQUENCE 121 AA; 13656 MW; 38EE4658 CMC32;
 Query Match 24.9%; Score 171.5; DB 1; Length 121;
 Best Local Similarity 37.1%; Pred. No. 6.1e-10;
 Matches 49; Conservative 18; Mismatches 52; Indels 13; Gaps 4;
 QY 1 mdptapsrallllllflhlaflgrspplsgpsasalsrsglqeqnqhgykrlselqve 60
 DB 1 MDLQKVPQMTLLFLFLNLSPLGSHPLSPSSQSP--EOSTWQKLELTREKSEENAQR 58
 QY 61 qtslepldesprptgvkksrevategrghkmvlyllrprspkmwqsgscfgirkndri 120
 DB 59 Q-----LSKDGPR-----KELKRVLRSDSAPFRIGERL-RNSKMAHSSSCFCQKIDRI 107
 QY 121 ssssglqckvrlr 132
 DB 108 GAVSRIGCDGLR 119
 RESULT 6
 ANFB_MOUSE STANDARD; PRT; 121 AA.
 ID ANFB_MOUSE
 AC P40753;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE BRAIN NATRIURETIC PEPTIDE PRECURSOR (BNP).
 GN NPPB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-BALB/C; TISSUE-HEART;
 RC MEDLINE; 94237953.
 RA OGAWA Y., ITOH H., TAMURA N., SUGA S., YOSHIMASA T., UEHIRA M.,
 RA MATSUDA S., SHONO S., NISHIMOTO H., NAKAO K.;
 RT "Molecular cloning of the complementary DNA and gene that encode
 mouse brain natriuretic peptide and generation of transgenic mice
 that overexpress the brain natriuretic peptide gene.";
 RL J. Clin. Invest. 93:1911-1921(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN-BALB/C;
 RC MEDLINE; 93238395.
 RA STEINHEIDER M.E.;
 RT "Structure, expression, and genomic mapping of the mouse natriuretic
 peptide type-B gene.";
 RL Circ. Res. 72:984-992(1993).
 CC [1-] FUNCTION: ACTS AS A CARDIAC HORMONE WITH A VARIETY OF BIOLOGICAL
 ACTIONS INCLUDING NARIURETICS, DIURETICS, VASORELAXATION, AND
 INHIBITION OF RENIN AND ALDOSTERONE SECRETION. IT IS THOUGHT TO
 PLAY A KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS.
 CC [1-] ALTERNATIVE PRODUCTS: A SHORTER FORM (ONE AMINO ACID LESS) IS
 GENERATED BY ALTERNATIVE SPLICING.
 CC [1-] TISSUE SPECIFICITY: EXPRESSED ABUNDANTLY IN THE VENTRICLE, AND IN
 A LESSER EXTENT IN THE ATRIUM.
 CC [1-] SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
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 CC EMBL; D16497; BAA03948.1; -;
 DR EMBL; S58667; CAB31712.1; -;
 DR MGD; MGI:97368; NPPB.

DR PROSITE: PS00263; NATRIURETIC_PEPIDE: 1.
DR Pfam: PF00212; ANP: 1.
KM Vasoactive; Brain; Signal; Alternative splicing.
FT SIGNAL 1 26
FT PEPIDE 27 121
FT PEPIDE 77 121
FT DISULF 99 115
FT VASAPLIC 43 43
FT CONFLICT 27 27
FT CONFLICT 71 71
SQ SEQUENCE 121 AA; 13756 MM; 5548E822 CRC32;

Query Match 24.0%; Score 165.5; DB 1; Length 121;
Best Local Similarity 35.6%; Pred. No. 2.3e-09;
Matches 52; Conservative 20; Mismatches 33; Indels 41; Gaps 7;

OY 1 mdpgaprrallllllflhlaifgrshpspgssadletsglqgrnhlgklselgve 60
1 MDLKLVSOMILFLFLVLPISLPGHSHYPLGSSQSP-----QRMKRL--- 45
61 qtsleplgesprtyvkwstrev-----tegl-rgthkmv]---yllra---Dpsphm 106
Dd 45 ---LELINE-----KSEMAHQQLKLDGLTKEHPRVLRSGSGTLRVRQGRQNSKV 93
OY 107 vqsgcfigrkmdrlssssglgckvlr 132
Dd 94 THISSCFGHKIDRIGSVSRIGCNALK 119

RESULT 7
ANF_CHICK STANDARD: PRT; 140 AA.
AC P18908;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPIDE)
DE (ANP) (PREPRONATRIODILATIN).
GN NPPA.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
CC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RX SEQUENCE FROM N.A.
RX MEDLINE: 91192169.
RA AKIZUKI N., KANGAWA K., MINAMINO N., MATSUO H.;
RA "Cloning and sequence analysis of complementary DNA encoding a
precursor for chicken natriuretic peptide.";
RA FEBS Lett. 280:357-362(1991).
RN [2]
RN SEQUENCE OF 112-140.
RP TISSUE=HEART;
RC MEDLINE: 89025805.
RX MIYATA A., MINAMINO N., KANGAWA K., MATSUO H.;
RX "Identification of a 29-amino acid natriuretic peptide in chicken
heart.";
RL Blochem. Biophys. Res. Commun. 155:1330-1337(1988).
CC -1- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE
SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
ACTIVITY.
CC -1- MISCELLANEOUS: A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF
ARRIOPEPTINS.
CC -1- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.

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CC -----
DR EMBL: X57702; -; NOT_ANNOTATED_COS.
DR PIR: S14320; S14320.
DR PIR: A31509; A31509.
DR PROSITE: PS00263; NATRIURETIC-PEPTIDE; 1.
DR PFAM: PF00212; ANP; 1.
KW Vasoactive; Signal.
FT SIGNAL 1
FT PEPTIDE 112 140 ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).
FT DISULFID 118 134
SQ SEQUENCE 140 AA; 15714 MW; E0A8F52F CRC32;

Query Match 19.9%; Score 137; DB 1; Length 140;
Best Local Similarity 29.9%; Pred. No. 1.5e-06;
Matches 43; Conservative 29; Mismatches 58; Indels 14; Gaps 4.

Oy 1 mdpgtapsrta1111flhaifgrtshp1sgpsasadtsg1qegrh1gqk1s----- 56
Db 1 MDRSSFSFGCLLLLTQLQ--PSANPYINSPAKEL--ASMEALLEEDKFALEIYL 56
Oy 56 ----elqveqtale1p1gesp1ptykwr-ewateg1g1ghrkmvlytl1ap1spkmgvgs 110
Db 57 ESNPLGEPGQGE1PELTDSDSQKAPKLA5MTPLSRNPF1KRLG1VGMFRMRDS 116
Oy 111 gcfgrtkmdr1sssg1gckv1trh 134
Db 117 GCFGRIRDRIGSLSGMCGNGSRKN 140

RESULT 8
ANF_CANFA STANDARD; PRT: 149 AA.
AC ANF_CANFA
AC P07499;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
DE (ANP) (PREPROMATRIODILATIN).
GN NPFA.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Canidae; Canis.
RN [1]
RX SEQUENCE FROM N.A.
RX MEDLINE: 86076957.
RA OKAWA S., IMAI M., IMIZUKA C., TAMARAGI Y., NAKAZATO H., MATSUO H.;
RT "Structure of dog and rabbit precursors of atrial natriuretic
RT polypeptides deduced from nucleotide sequence of cloned cDNA.";
RL Biochem. Biophys. Res. Commun. 132:892-899(1985).
CC -1- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE
CC SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
CC KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A GMP-STIMULATING
CC ACTIVITY.
CC -1- MISCELLANEOUS: A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF
CC ATRIOPEPTIN.
CC -1- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
CC -----
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CC -----
DR EMBL: M12045; AAA30828.1; -.
DR PIR: A25302; AMDG.
DR PROSITE: PS00263; NATRIURETIC-PEPTIDE; 1.
DR PFAM: PF00212; ANP; 1.
KW Vasoactive; Signal.
FT SIGNAL 1
FT PEPTIDE 122 149 ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANP).

```


Qy 60 eqstleipqdesrpt-----gwwksrevategrlgnkmylv-----lr 99
Db 70 ERALSLPEVPPTGWNPNQRDGCALGGSGMSDSD-----RSALLKSKRLAALLA 120

Oy 100 apispkmvgsqscfgfkrmdrtissssglgcxvlr 132
Db 121 APRS---LRSSCFGRMDRIGASOGLGCSNFR 150

RESULT 11

ID	ANF_HUMAN	STANDARD;	PRT;	153 AA.
AC	P01160;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	15-DEC-1998 (Rel. 37, Last annotation update)			
DE	ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE (ANP)) (PREPRONATRIODIATIN)).			
NC	NPFA OR PND.			
OC	Homo sapiens (Human).			
CC	Eumaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
RN	[1]			
RP	SEQUENCE OF 1-151 FROM N.A.			
RX	MEDLINE; 84219799.			
RA	OIKAWA S., IMAI M., UENO A., TANAKA S., NOGUCHI T., MAKAZATO H., KANGAWA K., FUKUDA A., MATSUO H.;			
RT	"Cloning and sequence analysis of cDNA encoding a precursor for human atrial natriuretic polypeptide.";			
RL	Nature 309:724-726(1984).			
RN	[2]			
RP	SEQUENCE OF 1-151 FROM N.A.			
RX	MEDLINE; 84295577.			
RA	NAKAYAMA K., OHKUBO H., HIROSE T., INAYAMA S., NAKANISHI S.;			
RT	"mRNA sequence for human cardiolitin-atrial natriuretic factor precursor and regulation of precursor mRNA in rat atria.";			
RL	Nature 310:699-701(1984).			
RN	[3]			
RP	SEQUENCE OF 1-151 FROM N.A.			
RX	MEDLINE; 85061626.			
RA	NEHER M., CAMBERLAND M., STROIS D., ARGENTIN S., DROVIN J., DIXON R.A.F., ZIVIN R.A., CONDRA J.H.;			
RT	"Gene structure of human cardiac hormone precursor, pronatriodilatin.";			
RL	Nature 312:654-656(1984).			
RN	[4]			
RP	SEQUENCE OF 1-151 FROM N.A.			
RX	MEDLINE; 85061627.			
RA	GREENBERG B.D., BENGEN G.H., SELHAMER J.J., LEWICKI J.A., FIDDES J.C.;			
RT	"Nucleotide sequence of the gene encoding human atrial natriuretic factor precursor.";			
RL	Nature 312:656-658(1984).			
RN	[5]			
RP	SEQUENCE OF 1-151 FROM N.A.			
RX	MEDLINE; 85065766.			
RA	SEIDMAN C.E., BLOCH K.D., KLEIN K.A., SMITH J.A., SEIDMAN J.G.;			
RT	"Nucleotide sequences of the human and mouse atrial natriuretic factor genes.";			
RL	Science 226:1206-1209(1984).			
RN	[6]			
RP	SEQUENCE OF 1-151 FROM N.A.			
RA	ERRINGTON H.;			
RL	Submitted (MAY-1998) to the EMBL/GenBank/DDJ databases.			
RN	[7]			
RP	SEQUENCE OF 118-153 FROM N.A.			
RX	MEDLINE; 85038509.			
RA	ZIVIN R.A., CONDRA J.H., DIXON R.A.F., SEIDAH N.G., CHRETIEN M., NEHER M., CAMBERLAND M., DROVIN J.;			
RT	"Molecular cloning and characterization of DNA sequences encoding rat and human atrial natriuretic factors.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 81:6325-6329(1984).			

Db 70 AGAALSPLEVPMTGEVSPAORDGALRGPMWSSD-----RSALLSKRLALLT 120

Qy 100 APTSPKMGVSGCGFRKMDRISSSSGLGCKVLR 132

Db 121 APRS---LRSSCGFGMDRIGAGSLGCSNFR 150

RESULT 12

ANF_PIG STANDARD: PRT: 150 AA.

AC P24259;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
DE (ANF) (PREPRONATRIODILATIN).
NPPA.

Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

CC [1]
RN SEQUENCE FROM N.A.
RC TISSUE-HEART RIGHT ATRIUM;
RX MEDLINE: 91067478.
RA MAEGERT H.J., APPELHANS H., GASSEN H.G., FORSSMANN W.G.;
RT "Nucleotide sequence of a porcine prepro atrial natriuretic peptide (ANF) cDNA."
RL Nucleic Acids Res. 18:6704-6704(1990).
RN [2]
RN SEQUENCE OF 25-150.
RC TISSUE-HEART RIGHT ATRIUM;
RX MEDLINE: 85124561.
RA FORSSMANN W.G., BIRR C., CARLOUST M., CHRISTMANN M., FINKE R.,
RA HENSCHEN A., HOCK D., KIRCHHEIM H., KREYE V., LOTSPEICH F., METZ J.,
RA MOTT V., REINCKE M.;
RT "The atricular myocardiocytes of the heart constitute an endocrine organ. Characterization of a porcine cardiac peptide hormone, atrial natriuretic peptide-126."
RL Cell Tissue Res. 238:425-430(1984).

CC -1- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE
SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
ACTIVITY.
CC -1- MISCELLANEOUS: A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF
ATRIOPEPTINS.
CC -1- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.

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CC EMBL: X54669; CAA38480.1; -
CC PIR: S13107; S13107.
DR PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
DR PFAM: PF00212; ANP; 1.
KW Vasoactive; Signal.
FT SIGNAL 1 24
FT PEPTIDE 25 54
FT (BY SIMILARITY).
FT CARDIODILATIN-RELATED PEPTIDE (CDP)
FT PEPTIDE 123 150
FT DISULFID 129 145
FT SEQUENCE 150 AA; 16351 MW; 4FR67B94 CRC32;
FT ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANF).

Query Match 15.9%; Score 109.5; DB 1; Length 150;
Best Local Similarity 33.8%; Pred. No. 0.0007;
Matches 50; Conservative 17; Mismatches 46; Indels 35; Gaps 10;

Qy 11 11111flaf1g-grshlp1gspgsasql1eqgrnhlgk-----1sel 57

Db 11 LVLVLF---QFGGTRANPV---YGSVSNADLMDFKNLLDHEKMKPLEDEAMPQVLSQ 65

Qy 58 qve-qtslep1qesprptgvk--srevateglrg----hrkmvlyt-----1raprp 104

Db 66 NEVVGAPLSPLLEVPPMTGEVNPAPARDGALG-RQPMWSDRSALLSKRLALLAAPRS- 124

Qy 105 kmvgsgcgrkmdrissssglgckvlt 132

Db 124 --LRSSCGFGMDRIGAGSLGCSNFR 149

RESULT 13

ANF_RABIT STANDARD: PRT: 153 AA.

AC P07500;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
DE (ANF) (PREPRONATRIODILATIN).
NPPA.

Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Lagomorpha; Leporidae; Oryctolagus.

CC [1]
RN SEQUENCE FROM N.A.
RX MEDLINE: 86076957.
RA OIKAWA S., IMAI M., INUZUKA C., TAMARAGI Y., NAKAZATO H., MATSUO H.;
RT "Structure of dog and rabbit precursors of atrial natriuretic
polypeptides deduced from nucleotide sequence of cloned cDNA."
RL Biochem. Biophys. Res. Commun. 132:892-899(1985).

CC -1- FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE
SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
ACTIVITY.
CC -1- MISCELLANEOUS: A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF
ATRIOPEPTINS.
CC -1- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.

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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

CC EMBL: M12046; AAA31162.1; -
CC PIR: B25302; AMRB.
DR PROSITE: PS00263; NATRIURETIC_PEPTIDE; 1.
DR PFAM: PF00212; ANP; 1.
KW Vasoactive; Signal.
FT SIGNAL 1 25
FT PEPTIDE 124 151
FT DISULFID 130 146
FT SEQUENCE 153 AA; 16843 MW; 1FA4FB42 CRC32;
FT ATRIAL NATRIURETIC PEPTIDE, ALPHA (ANF).

Query Match 15.3%; Score 105.5; DB 1; Length 153;
Best Local Similarity 28.4%; Pred. No. 0.0017;
Matches 44; Conservative 20; Mismatches 42; Indels 49; Gaps 8;

Qy 11 11111flaf1ggrshlp1gspgsasql1eqgrnhlgk-----1selg 58

Db 12 LFCIAFWHPD1G--ANPVNAMSADL--MDFKNLLDHEDRMFEDEAVPPALSPQS 67

Qy 59 veg-tslepl1qesprpt-----vwksrevateglrghkmvlyt----- 98

Db 68 DEAGALSPLEVPMTGEVSPAORDGALGRSTWEASE-----RSALLSKRLAL 118

Qy 98 lraprpkmvgsgcgrkmdrissssglgckvlt 132


```

DB 119 LTRPRS---LRSSCTGGRIDRIGAGSLGCNSFR 150

RESULT 14
ID ANF_RANCA STANDARD; PRT; 145 AA.
AC P18909:
DT 01-NOV-1990 (rel. 16, Created)
DT 01-MAR-1992 (rel. 21, Last sequence update)
DT 01-FEB-1995 (rel. 31, Last annotation update)
DE ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
OS (ANP).
DE Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Raninae; Rana.
RN [1]
RP SEQUENCE FROM N.A.
RA KOJIMA M.;
RP Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.
(2)
KP SEQUENCE OF 122-145.
RC TISSUE=HEART;
RX MEDLINE; 89025806.
RA SAKATA J., KANGAWA K., MATSUO H.;
RT Identification of new atrial natriuretic peptides in frog heart.;
RL Biochem. Biophys. Res. Commun. 155:1338-1345(1988).
CC - FUNCTION: VASOACTIVE ACTIVITY. HAS A CGMP-STIMULATING ACTIVITY.
CC - SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
CC CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sdb.ch/announce/
CC or send an email to license@sdb-sdb.ch).
CC -----
DR EMBL; D01043; BA00850.1; -
DR PIR; A31510; A31510.
DR PROSITE; P500263; NATRIURETIC_PEPTIDE; 1.
DR PFAM; PF00212; ANP; 1.
KW Vasoactive; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT PEPTIDE 122 145 ATRIAL NATRIURETIC FACTOR.
FT DISULFID 125 141
FT SEQUENCE 145 AA; 15934 MW; 6A1FA352 CRC32;

Query Match 15 1%; Score 104; DB 1; Length 145;
Best Local Similarity 28.8%; Pred. No. 0.0023;
Matches 42; Conservative 19; Mismatches 43; Indels 42; Gaps 7;

QY 12 llllflhflgrrshpplgspgsasdl-etsqldqgrnhlgklselqyqstleplq-- 69
DB 9 ltrvllllhltkrgrgprvnsplssdlsdkglr---ledrlpvev---trvqdi 61
QY 69 -----esprp-----tgvwksrevateglgthrkmylytlrapt 102
DB 62 fapnydsadsnsapsfltevarpgradmymnrgsmwtqoekrsp-----lrrkrlrellnapt 117
QY 103 spkmvgsgcfcgrkmdrissssglgc 128
DB 118 S--WRRSSDCFGSRIDRIGAGSLGCNSFR 141

RESULT 15
ANF_MOUSE STANDARD; PRT; 152 AA.
AC P05125;
DT 13-AUG-1987 (rel. 05, Created)
DT 13-AUG-1987 (rel. 05, Last sequence update)

DB 01-OCT-1996 (rel. 34, Last annotation update)
DE ATRIAL NATRIURETIC FACTOR PRECURSOR (ANF) (ATRIAL NATRIURETIC PEPTIDE)
OS (ANP) (PREPRONATRIODILATIN).
GN NPFA OR PND.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85065766.
RA SEIDMAN C.E., BLOCH K.D., KLEIN K.A., SMITH J.A., SEIDMAN J.G.;
RT "Nucleotide sequences of the human and mouse atrial natriuretic
RT factor genes."
RL Science 226:1206-1209(1984).
CC - FUNCTION: ATRIAL NATRIURETIC FACTOR (ANF) IS A POTENT VASOACTIVE
CC SUBSTANCE SYNTHESIZED IN MAMMALIAN ATRIA AND IS THOUGHT TO PLAY A
CC KEY ROLE IN CARDIOVASCULAR HOMEOSTASIS. HAS A CGMP-STIMULATING
CC ACTIVITY.
CC - MISCELLANEOUS: A DISULFIDE BOND IS REQUIRED FOR FULL ACTIVITY OF
CC ATRIOPEPTINS.
CC - SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
CC CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sdb.ch/announce/
CC or send an email to license@sdb-sdb.ch).
CC -----
DR EMBL; K02781; AAA37235.1; -
DR PIR; A29370; AMNS.
DR MGD; MGI:97367; NPRA.
DR PROSITE; P500263; NATRIURETIC_PEPTIDE; 1.
DR PFAM; PF00212; ANP; 1.
KW Vasoactive; Signal.
FT SIGNAL 1 24
FT PEPTIDE 126 149 AURICULIN A (BY SIMILARITY).
FT PEPTIDE 126 150 AURICULIN B (BY SIMILARITY).
FT PEPTIDE 127 149 ATRIOPEPTIN I (BY SIMILARITY).
FT PEPTIDE 127 147 ATRIOPEPTIN II (BY SIMILARITY).
FT DISULFID 129 145 BY SIMILARITY.
FT SEQUENCE 152 AA; 16645 MW; 5163CB23 CRC32;

Query Match 14.5%; Score 100; DB 1; Length 152;
Best Local Similarity 31.2%; Pred. No. 0.0058;
Matches 48; Conservative 19; Mismatches 51; Indels 36; Gaps 9;

QY 8 srallllflhflaf-1grf--shpplgspgsasdl-etsqldqgrnhlgk----- 54
DB 3 sfsitlgfvlvafwlpghlganpvisavsnldl--mfrknlldhleeampvedevmpq 60
QY 54 -ltselqveq--tsleplgesprltgvwksrevateglgrh-----kmvlytl 98
DB 61 alse-qteagaaalselpvpmwtg--evnplpbgasarspmpwpsdrsalrksrlrat 117
QY 99 raprpskxmgvgsgcfcgrkmdrissssglgcxvlr 132
DB 118 LA--GPRSLRRSSCTGGRIDRIGAGSLGCNSFR 149

Search completed: April 27, 2000, 21:53:43
Job time: 12259 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 27, 2000, 18:34:48 ; Search time 493.05 Seconds
(without alignments)
3078.424 Million cell updates/sec

Title: SEQ1
Perfect score: 402
Sequence: 1 atggatcccccagacagcacc.....gcaagtcgtgagcgccat 402

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4538634 seqs, 1887831982 residues
1 number of hits satisfying chosen parameters: 9077268

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : EST:*
1: em_est1:*
2: em_est2:*
3: em_est3:*
4: em_est4:*
5: em_est5:*
6: em_est6:*
7: em_est7:*
8: em_est8:*
9: em_est9:*
10: em_est10:*
11: em_est11:*
12: em_est12:*
13: em_est13:*
14: em_est14:*
15: em_est15:*
16: em_est16:*
17: em_est17:*
18: em_est18:*
19: em_est19:*
20: gb_est1:*
21: gb_est2:*
22: gb_est3:*
23: gb_est4:*
24: gb_est5:*
25: gb_est6:*
26: gb_est7:*
27: gb_est8:*
28: gb_est9:*
29: gb_est10:*
30: gb_est11:*
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99: gb_gss10:*
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101: em_gss12:*
102: gb_gss12:*
103: gb_gss13:*
104: gb_gss14:*
105: gb_gss15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	287.6	71.5	360	30	AA216038	AA216038 hp0251.se
2	258.4	64.3	371	30	AA216138	AA216138 hp0519.se

FEATURES	
Source	Location/Qualifiers
	1..360
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone_lib="Human fetal heart, Lambda ZAP Express"
	/lab_host="E. coli XL1-Blue"
	/note="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2: XhoI; mRNA was purified from human fetal hearts (8-10 weeks). cDNA was synthesized using a XhoI-Oligo dT adaptor-primer. EcoRI adaptors were ligated, followed by digestion with XhoI, for directional cloning, into predigested Lambda ZAP Express."
BASE COUNT	66 a 110 c 118 g 66 t
ORIGIN	
Query Match	71.5%; Score 287.6; DB 30; Length 360;
Best Local Similarity	94.7%; Pred. No. 2,2e-61;
Matches 341; Conservative 0; Mismatches 14; Indels 5; Gaps 4	
Db 45	ctcttcgcatcgtggtcttcctggagagtcgtccca-ccgctgaggcagcccggttcag 103
Db 1	ctctgcgcgctctgctgcttctctggagagtcgtcccaaccctgaggagccccggttcag 60
Db 104	cctcgagcttggaaaagtcgaggtctacagagagacagcaaacatttgcaggccaacgtc 163
Db 61	ctctgcgacttggaaaagtcgaggttcaagagagacagcgaacatttgcaggccaacgtc 120
Db 164	cggagctgcagagtgaggagacagacatccctg-gagccctccagagagacccccgtccaca 222
Db 121	cggagctgcagagtgaggagacacatccctgtgtgagcccccttccagagagacccccgtccaca 180
Db 223	ggtgtc--tggaaagtcctccggagagtagccaccagagagcatcctgtgtggcacccgcaaatg 280
Db 181	gggtgtgtgtaagttccccggagagtagccaccagagagcatcctgtgtggcacccgcaaatg 240
Db 281	tctcttaaacctcggaggagacacagaaaccccaaga-tggtgcaaggtgtcgtgtgttt 339
Db 241	tgccttaaacctcgtgtggagacacagaaaccccaaatgtgtgacaaaggtctcgtgtgttt 300

Db 30

RESULT 2

LOCUS	AA216138				
DEFINITION	AA216138	371 bp	mRNA	EST	04-FEB-1997
ACCESSION	hp0519.seq.F	Human fetal heart,	Lambda ZAP Express	Homo sapiens	
VERSION	CDNA 5',	mRNA sequence.			
KEYWORDS	AA216138				
SOURCE	AA216138.1	GI:1816077			
ORGANISM	EST.				
REFERENCE	human.				
AUTHORS	Homo sapiens				
TITLE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;				
JOURNAL	Eutheria; Primates; Carnivora; Homnidae; Homo.				
COMMENT	1 (bases 1 to 371)				
	Llew.C.C.				
	CDNAs from fetal heart (1996)				
	Unpublished (1996)				
	On Sep 12, 1996 this sequence version replaced gl:1326684.				
	Contact: Llew CC				
	Department of Laboratory Medicine and Pathobiology				
	University of Toronto				
	Banting Institute, 100 College St., Toronto, Ontario, M5G1L5				
	Tel: 4169788758				
	Fax: 4169785650				
	Email: llew@centcc.utoronto.ca				
	PCR Primers				

FORWARD: 5' GCCAAGCTCGAATTACCTCACTAAAGG 3'
 BACKWARD: 5' CCAGTGAATGTATACGACTCACTATAGGCG 3'
 Seq primer: 5' GAATTACCTCACTAAAGG 3'

FEATURES

source

1..371
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="Human fetal heart, Lambda ZAP Express"
 /lab_host="E. coli XL1-Blue"
 /note="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2: XhoI; mRNA was purified from human fetal hearts (8-10 weeks). cDNA was synthesized using a XhoI-Oligo dt adaptor-primer. EcoRI adaptors were ligated, followed by digestion with XhoI for directional cloning into predigested Lambda ZAP Express."

BASE COUNT
 ORIGIN

73 a 126 c 115 g 57 t

Query Match

Best Local Similarity 99.38; Pred. No. 3,4e-54; Length 371;
 Matches 270; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 atggtatccagagacagacacccctccggcgctcctgtctcctcttcttgcacatgct 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 100 ATGATCCCCAGACAGACACCTTCCGGGCGCTCTCTGCTCTTCTTCTGATCTGCT 159
 QY 61 ttctctggaggtcgtctccaccgccttggcagcccggttcaagcttggacttggaaacg 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 160 TTCTGGGAGGTGCTTCCACCCCGTGGGAGCCCGGTTCAGCTCGACTTGGAAACG 219
 QY 121 tcgggttaacagagcagcagcaacatttgaggagcaactgtggagctcagttgag 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 220 TCCGGTTACAGAGAGCGACGACCATTTGAGGCAAACTGTGAGACTCAGGTGAG 279
 QY 181 cagacatccctggagacccctccagagagcccgctcccaaggtgtc-tgaaatcccg 239
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 280 CAGACATCCCTGGAGGCCCTCCAGAGAGGCCCGCTCCCAAGGCTTTGAGAGTCCG 339
 QY 240 ggaagtagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 271
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 340 GGAGTAGCCACGAGGCGATCGTTGGCACC 371

RESULT 3

N85365

LOCUS

DEFINITION

J3336F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA

clone J3336 5' similar to NATRIURETIC PEPTIDE PRECURSOR, mRNA

sequence.

ACCESSION

N85365

VERSION

N85365.1

KEYWORDS

EST.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

500 bp mRNA 01-APR-1996
 Human fetal heart, Lambda ZAP Express Homo sapiens cDNA
 clone J3336 5' similar to NATRIURETIC PEPTIDE PRECURSOR, mRNA
 sequence.
 N85365
 N85365.1 GI:1260990
 EST.
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Llew.C.C.
 CDNA's from fetal heart (1996)
 Unpublished (1996)
 On May 8, 1995 this sequence version replaced gi:800920.
 Contact: Llew CC
 Department of Laboratory Medicine and Pathobiology
 University of Toronto
 Banting Institute, 100 College St., Toronto, Ontario, M5G1L5
 Tel: 4169788758
 Fax: 4169785650
 Email: llewcc@utcc.utoronto.ca
 Seq primer: GAATTACCTCACTAAAGG.
 Location/Qualifiers
 1..500
 /organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="3336"

/lab_host="E. coli XL1-Blue"

/note="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2: XhoI; mRNA was purified from human fetal hearts (8-10 weeks). cDNA was synthesized using a XhoI-Oligo dt adaptor-primer. EcoRI adaptors were ligated, followed by digestion with XhoI for directional cloning into predigested Lambda ZAP Express."

BASE COUNT
 ORIGIN

106 a 161 c 145 g 88 t

Query Match 58.08; Score 233; DB 25; Length 500;
 Best Local Similarity 92.18; Pred. No. 7e-48;
 Matches 279; Conservative 0; Mismatches 20; Indels 4; Gaps 3;

QY 1 atggtatccagagacagacacccctccggcgctcctgtctcctcttcttgcacatgct 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 99 ATGATCCCCAGACAGACACCTTCCGGGCGCTCTCTGCTCTTCTTCTGATCTGCT 158
 QY 61 ttctctggaggtcgtctccaccgccttggcagcccggttcaagcttggacttggaaacg 120
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 Db 159 TTCTGGGAGGTGCTTCCACCCCGTGGGAGCCCGGTTCAGCTCGACTTGGAAACG 218
 QY 121 tcgggttaacagagcagcagcaacatttgaggagcaactgtggagctcagttgag 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 219 TCCGGTTACAGAGAGCGCG- AACCATTTGACAGGCAAACTGTGAGACTCAGGTGAG 277
 QY 181 cagacatccctggagacccctccagagagcccgctcccaaggtgtc-tgaaatcccg 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 278 CAGACATCCCTGGAGGCCCTCCAGAGAG- CCGCTCCACAGGTGCTTGAAGTCC- G 334
 QY 241 ggaagtagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 335 GGAATACCAACGAGGCGATCGTGGAGCCCAAAATGATCCCTTAACTCGGAGACA 394
 QY 301 cca 303
 |||||
 Db 395 CGA 397

RESULT 4

AA216173

LOCUS

DEFINITION

hp0589.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens

cDNA 5', mRNA sequence.

ACCESSION

AA216173

VERSION

AA216173.1

KEYWORDS

EST.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

279 bp mRNA 04-FEB-1997
 Human fetal heart, Lambda ZAP Express Homo sapiens
 cDNA 5', mRNA sequence.
 AA216173
 AA216173.1 GI:1816112
 EST.
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Llew.C.C.
 CDNA's from fetal heart (1996)
 Unpublished (1996)
 On Sep 12, 1996 this sequence version replaced gi:1288232.
 Contact: Llew CC
 Department of Laboratory Medicine and Pathobiology
 University of Toronto
 Banting Institute, 100 College St., Toronto, Ontario, M5G1L5
 Tel: 4169788758
 Fax: 4169785650
 Email: llewcc@utcc.utoronto.ca
 PCR primers
 FORWARD: 5' GCCAAGCTCGAATTACCTCACTAAAGG 3'
 BACKWARD: 5' CCAGTGAATGTATACGACTCACTATAGGCG 3'
 Seq primer: 5' GAATTACCTCACTAAAGG 3'.
 Location/Qualifiers
 1..279
 /organism="Homo sapiens"

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human fetal heart, Lambda ZAP Express"
/lab_host="E. coli XL1-Blue"
/notes="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2:
XhoI; mRNA was purified from human fetal hearts (8-10
weeks). cDNA was synthesized using a XhoI-Oligo dr
adaptor primer. EcoRI adaptors were ligated, followed by
digestion with XhoI, for directional cloning into
predigested Lambda ZAP Express."

```

BASE COUNT

```

59 a 80 c 93 g 47 t

```

ORIGIN

```

Query Match 54.7%; Score 219.8; DB 30; Length 279;
Best Local Similarity 98.1%; Pred. No. 9.9e-45;
Matches 254; Conservative 0; Mismatches 2; Indels 3; Gaps 3;

```

```

146 attgagggcaaacgtgtcgagctgaggtgagcagacatccctggagccctcagg 205
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1 ATTTGAGGGCAAACTGTCTGAGCTGAGTGGAGCAGACATCCTTGAGCCCTCAGG 60
|||||
QY 206 agagccccccgtcccaaggtgtctggaagtcgccggaggtagccacgagggcatcgtg 265
|||||
DB 61 AGAGCCCGCTCCACAGAGTGTGGAAGTCCGGAGAGTACGACGAGGCGATCCGTG 120
|||||
QY 266 ggcacggcaaaatggtctc-tacacctggcgagcaccacgaagcccaagatggtgcga 324
|||||
DB 121 GGCACGCAAAATAGTCTTACCTTACCTGCGGACACGAAAGCCCAAGATGATACAA 180
|||||
QY 325 gggctc-tggctgtcttggagagaatgagaccgagatcagctcctcagtggtgctg 383
|||||
DB 181 GGGTCTTGCTGCTTTGGAGGAAGATGACGCGATCAGTCTCTCAAGTGGCTGGGCTG 240
|||||
QY 384 caaatgctgagggcgat 402
|||||
DB 241 C-AAGTGTGAGGCGGCGAT 258
|||||

```

RESULT 5

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AI634108/c 425 bp mRNA EST 26-APR-1999
LOCUS wa88a04.x1 NCI-CGAP_G66 Homo sapiens cDNA clone IMAGE:2303214 3'
DEFINITION similar to gb:M25296 BRAIN NATURETIC PEPTIDE PRECURSOR (HUMAN);
MRA sequence.
AI634108
ACCESSION AI634108.1 GI:4685438
VERSION EST.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 425)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncigap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On May 18, 1998 this sequence version replaced gi:1138182.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldi, Ph.D.
cDNA library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/URL at:
www.bio.lnl.gov/bhrp/image/image.html

```

```

Seq primer: -40UP from Gibco
High quality sequence stop: 348.

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FEATURES

```

Location/Qualifiers
1..425
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="2303214"
/clone_lib="NCI-CGAP_G66"
/tissue_type="Pooled germ cell tumors"
/lab_host="DH10B"
/notes="Vector: pRTT3-Pac (Pharmacia) with a modified
polylinker. Plasmid DNA from the normalized library
NCI-CGAP_G64 was prepared, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from a pool of 5,000 clones made
from the same library (cloneIDs 1257096-1258631,
146064-1470983, and 1475592-1476743). Subtraction by
Bento Soares and M. Fatima Bonaldi."

```

BASE COUNT

```

114 a 109 c 103 g 97 t 2 others

```

```

Query Match 46.7%; Score 187.8; DB 49; Length 425;
Best Local Similarity 95.1%; Pred. No. 9e-37;
Matches 214; Conservative 0; Mismatches 9; Indels 2; Gaps 2;

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QY 178 ggcagacatccctgagccctccagagagcccgctccacaggtgtctgagctcc 237
|||||
DB 425 GAGCAGACATCTTGTGAGGCTTTCAGNAGAGCCCGTCCACAGGTGTGNAAGTCC 366
|||||
QY 238 cggaggtagccacccgagggcatccgtggcgacgcgaatgtctctaacctcg 297
|||||
DB 365 CGGAGGTAGCCACGAGGCGATCCGTGGGACCAAAATGTCTCTT-CACCTTGGCG 307
|||||
QY 298 gaccacgaagcccaagatggtgaaaggtgtgtgtctgttggaggaagatgagccg 357
|||||
DB 306 GCACC-CGAAGCCCAAGATGAGTGTGCAAGGCTGTGCTTTGGAGGAAGATGAGACCGG 248
|||||
QY 358 atcagctcctccagtggtgctgcaaaagtgtctgagggcgat 402
|||||
DB 247 ATCAGCTCTCTCCAGTGGCTGGGCTGCAAAAGTGTGAGGCGGCGAT 203
|||||

```

RESULT 6

```

AA216210 228 bp mRNA EST 04-FEB-1997
LOCUS hp0679.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens
DEFINITION cDNA 5', mRNA sequence.
ACCESSION AA216210
VERSION AA216210.1 GI:1816149
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 228)
Liew,C.C.
cDNAs from fetal heart (1996)
Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1287882.
Contact: Liew CC
Department of Laboratory Medicine and Pathobiology
University of Toronto
Banting Institute, 100 College St., Toronto, Ontario, M5G1L5
Tel: 4169788758
Fax: 4169785650
Email: liew@utoronto.ca
PCR Primers
FORWARD: 5' GCAAGCTCGAATTAACCTCCTACTAAGG 3'
BACKWARD: 5' CCACTGATGTGATACGACTACTAAGGCG 3'
Seq primer: 5' GAATTAACCTCCTACTAAGG 3'.

```

FEATURES

```

Location/Qualifiers
1..228
/organism="Homo sapiens"

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normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NBH19W."

BASE COUNT 98 a 83 c 79 g 96 t

Query Match 35.8%; Score 144; DB 43; Length 356;
Best Local Similarity 100.0%; Pred. No. 5.2e-26;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 259 atccgtggcaccgcaaatggtctctacacccctgaggagcagcaagcccaatg 318
|||||
DB 356 ATCCGTGGCACCAGCAAAATGCTCTACACCTCGGGGACACAGCCCAATG 297
|||||
QY 319 gtgcaagggtctggtctcttggaggaagatgacggatcagctctccagtgcctg 378
|||||
296 GTGCAAGGCTGTGGCTCTTGGAGAGATGAGACCGGATCAGCTCTCCAGTGCCTG 237
|||||
QY 379 ggtcgtcaagtgctgagggagcat 402
|||||
DB 236 GGCTGCAAGTGTGAGGCGGCAT 213
|||||

RESULT 9 AA216011 333 bp mRNA EST 04-FEB-1997

LOCUS AA216011 hp0221.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens
DEFINITION CDNA 5', mRNA sequence.

ACCESSION AA216011 GI:1815966

VERSION AA216011.1

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

AUTHORS Eutheria; Primates; Catarrhini; Homiidae; Homo.

JOURNAL 1 (bases 1 to 333)

COMMENT CDNAs from fetal heart (1996)
Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1324710.

CONTACT: Lew CC

Department of Laboratory Medicine and Pathobiology

University of Toronto

Banting Institute, 100 College St., Toronto, Ontario, M5G1L5

Tel: 416/9788758

Fax: 416/9785650

Email: liewcc@utcc.utoronto.ca

PCR Primers

FORWARD: 5' GCCAAGCTCGAATTACCTCACTAAGG 3'

BACKWARD: 5' CCAGTGAATTGATGACCTCACTAAGG 3'

Seq primer: 5' GAATTACCTCACTAAGG 3'

Location/Qualifiers

1. 333

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="Human fetal heart, Lambda ZAP Express"

/lab_host="E. coli XL1-Blue"

/note="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2: XhoI; mRNA was purified from human fetal hearts (8-10 weeks). CDNA was synthesized using a XhoI-Oligo dt adaptor-primer. EcoRI adaptors were ligated, followed by digestion with XhoI, for directional cloning into predigested Lambda ZAP Express."

BASE COUNT 83 a 77 c 86 g 87 t

ORIGIN

Query Match 34.8%; Score 140; DB 30; Length 333;
Best Local Similarity 99.3%; Pred. No. 4.8e-25;
Matches 151; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 251 ccagggcatccgtgggacccgcaaatggtctctacacccctgaggagcagcaagcc 310
|||||

DB 1 CCAGGGCATCCGTGGGACCCGCAAAATGCTCTACACCTGCGGACACGAGCC 59
|||||

QY 311 ccaagatgtgcaagggtctggtctcttggaggaagatgacggatcagctctccaa 370
|||||
DB 60 CCAAGATGTGCAAGGCTGTGGCTCTTGGAGAGATGAGACCGATCAGCTCTCCA 119
|||||

QY 371 gtgctggtctgcaagtgctgagggagcat 402
|||||
DB 120 GTGCTGGGCTCAAGTGTCTGAGCGGCAT 151
|||||

RESULT 10 A1656014 296 bp mRNA EST 04-MAY-1999

LOCUS A1656014/c t142e12.x1 NCI-CGAP_G6 Homo sapiens CDNA clone IMAGE:2243470 3'
DEFINITION similar to gb:U25296 BRAIN NATURETIC PEPTIDE PRECURSOR (HUMAN);
mRNA sequence.

ACCESSION A1656014 GI:4739993

VERSION A1656014

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

AUTHORS Eutheria; Primates; Catarrhini; Homiidae; Homo.

JOURNAL 1 (bases 1 to 296)

COMMENT NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Index

Unpublished (1997)

On Jun 5, 1998 this sequence version replaced gi:3187756.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert.Strausberg@nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

CDNA library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/dbp/image/image.html

Seq primer: -40up from Gibco.

Location/Qualifiers

1. 296

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="NCI-CGAP_G6"

/clone_lib="NCI-CGAP_G6"

/tissue_type="pooled germ cell tumors"

/lab_host="PH10B"

/note="Vector: pT773D-Pac (Pharmacia) with a modified

polylinker; Plasmid DNA from the normalized library

NCI-CGAP_G64 was prepared, and ss circles were made in

vitro. Following RAP purification, this DNA was used as

tracer in a subtractive hybridization reaction. The driver

was PCR-amplified cDNAs from a pool of 5,000 clones made

from the same library (clones 1257096-1258631,

1469064-1470983, and 1475592-1476743). Subtraction by

Bento Soares and M. Fatima Bonaldo.

BASE COUNT 91 a 72 c 59 g 74 t

ORIGIN

Query Match 24.4%; Score 98; DB 49; Length 296;
Best Local Similarity 100.0%; Pred. No. 1e-14;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 296 GAAGCCCCAAGATGTCAGAGGTCCTGCTTTGGAGGAGATGACCGGATCAGCT 237
 QY 365 cctccagtgctgctgctgcaagtgctgagcgccat 402
 Db 236 CCTCAGTGGCTGGCTGCTGCAAGTCTGAGCGGCAT 199

RESULT 11
 AM197593 296 bp mRNA EST 29-NOV-1999
 LOCUS AM197593/c
 DEFINITION xnm44407.x1 NCI_CGAP_G6 Homo sapiens cDNA clone IMAGE:2687100 3'
 similar to gb:M25296 BRAIN NATRIURETIC PEPTIDE PRECURSOR (HUMAN);,
 mRNA sequence.

ACCESSION AM197593.1 GI:6476823
 VERSION AM197593
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutharia; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 296)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 On Jul 8, 1999 this sequence version replaced gi:5422539.
 COMMENT Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
 R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/dbp/image/image.html

JOURNAL On Jul 8, 1999 this sequence version replaced gi:5422539.
 COMMENT Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
 R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/dbp/image/image.html

FEATURES
 source
 Seq primer: -40UP from gibco.
 Location/Qualifiers
 1. 296
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="NCI_CGAP_G6"
 /tissue_type="pooled germ cell tumors"
 /lab_host="DH10B"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Plasmid DNA from the normalized library
 NCI_CGAP_G64 was prepared and ss circles were made in
 vitro. Following HAP purification, this DNA was used as
 tracer in a subtractive hybridization reaction. The driver
 was PCR-amplified cDNAs from a pool of 5,000 clones made
 from the same library (cloneds 1257096-1258631,
 1469064-1470983, and 1475592-1476743). Subtraction by
 Bento Soares and M. Fatima Bonaldo."

BASE COUNT 91 a 72 c 61 g 72 t
 ORIGIN

Query Match 24.4%; Score 98; DB 74; Length 296;
 Best Local Similarity 100.0%; Pred. No. 1e-14;
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 305 gaagcccaagatgctgcaaggtctgctgcttggaggaagatgacccgatacagct 364
 Db 296 GAAGCCCCAAGATGTCAGAGGTCCTGCTTTGGAGGAGATGACCGGATCAGCT 237
 QY 365 cctccagtgctgctgctgcaagtgctgagcgccat 402
 Db 236 CCTCAGTGGCTGGCTGCTGCAAGTCTGAGCGGCAT 199

RESULT 12
 A1656015 284 bp mRNA EST 04-MAY-1999
 LOCUS A1656015/c
 DEFINITION tt42f01.x1 NCI_CGAP_G6 Homo sapiens cDNA clone IMAGE:2243449 3'
 similar to gb:M25296 BRAIN NATRIURETIC PEPTIDE PRECURSOR (HUMAN);,
 mRNA sequence.

ACCESSION A1656015 GI:4739994
 VERSION A1656015
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutharia; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 284)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 On Jun 5, 1998 this sequence version replaced gi:3187757.
 COMMENT Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
 R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/dbp/image/image.html

JOURNAL On Jun 5, 1998 this sequence version replaced gi:3187757.
 COMMENT Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
 R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/dbp/image/image.html

FEATURES
 source
 Trace considered overall poor quality
 Seq primer: -40UP from gibco
 High quality sequence stop: 1.
 Location/Qualifiers
 1. 284
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="NCI_CGAP_G6"
 /tissue_type="pooled germ cell tumors"
 /lab_host="DH10B"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Plasmid DNA from the normalized library
 NCI_CGAP_G64 was prepared and ss circles were made in
 vitro. Following HAP purification, this DNA was used as
 tracer in a subtractive hybridization reaction. The driver
 was PCR-amplified cDNAs from a pool of 5,000 clones made
 from the same library (cloneds 1257096-1258631,
 1469064-1470983, and 1475592-1476743). Subtraction by
 Bento Soares and M. Fatima Bonaldo."

BASE COUNT 96 a 70 c 59 g 59 t
 ORIGIN

Query Match 17.4%; Score 70; DB 49; Length 284;
 Best Local Similarity 84.0%; Pred. No. 8e-08;
 Matches 79; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 309 ccccaagatgctgcaaggtctgctgcttggaggaagatgacccgatacagctc 368
 Db 280 CCAATATGTCGTCAGAGGTCCTGCTTTGGAGGAGATGACCGGATCAGCT 221
 QY 369 cagtgctgctgctgcaagtgctgagcgccat 402
 Db 220 CAATGCATGCTGCACAGTGTAGAGCGGCAT 187

RESULT 13
 AA799914/c
 LOCUS AA799914 337 bp mRNA EST 30-APR-1998

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 27, 2000, 20:16:48 ; Search time 21.65 Seconds
(without alignments)
2223.035 Million cell updates/sec

Title: SEQ1
Perfect score: 402
Sequence: 1 atgagtcgccagacagcacc.....gcaagtcgtcagcgccat 402

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 214294 seqs, 59861574 residues

Minimum number of hits satisfying chosen parameters: 428588

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/5C.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/5D.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/6.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCITUS9.COMB.seq:*
7: /cgn2_6/ptodata/1/ina/Dackfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	260.4	64.8	1519 4	US-08-850-910A-44 Sequence 44, Appl
2	182.2	45.3	707 4	US-08-850-910A-40 Sequence 40, Appl
3	139	34.6	1507 4	US-08-850-910A-38 Sequence 38, Appl
4	123.8	30.8	1504 4	US-08-850-910A-17 Sequence 17, Appl
5	116.4	29.0	1804 4	US-08-850-910A-42 Sequence 42, Appl
6	39.8	9.9	1926 1	US-08-278-728A-22 Sequence 22, Appl
7	39.8	9.9	1926 1	US-08-480-528A-9 Sequence 9, Appl
8	39.8	9.9	1926 2	US-08-643-563A-22 Sequence 22, Appl
9	39.8	9.9	1926 2	US-08-643-763A-22 Sequence 22, Appl
10	39.8	9.9	1926 2	US-08-462-623-22 Sequence 22, Appl
11	39.8	9.9	1926 2	US-08-451-953A-22 Sequence 22, Appl
12	39.8	9.9	1926 3	US-08-445-458A-22 Sequence 22, Appl
13	39.8	9.9	1926 4	US-08-461-397A-22 Sequence 22, Appl
14	39.8	9.9	1926 4	US-08-912-088-22 Sequence 22, Appl
15	38.2	9.5	1926 1	US-07-901-703-12 Sequence 12, Appl
16	38.2	9.5	1926 1	US-08-147-023-26 Sequence 26, Appl
17	38.2	9.5	1926 1	US-08-479-666-9 Sequence 9, Appl
18	38.2	9.5	1926 1	US-08-155-343A-22 Sequence 22, Appl
19	38.2	9.5	1926 1	US-08-406-672-22 Sequence 22, Appl
20	38.2	9.5	1926 2	US-08-447-570-26 Sequence 26, Appl
21	38.2	9.5	1926 3	US-08-459-346-7 Sequence 7, Appl
22	38.2	9.5	1926 3	US-08-901-200A-9 Sequence 9, Appl
23	38.2	9.5	1926 3	US-08-449-700-26 Sequence 26, Appl
24	38.2	9.5	1926 6	US-08-449-699A-26 Sequence 26, Appl
25	38.2	9.5	1926 6	PCT-US92-01968-22 Sequence 12, Appl
26	38.2	9.5	1926 6	PCT-US93-05446-12 Sequence 12, Appl
27	38.2	9.5	1926 6	PCT-US93-07189-7 Sequence 7, Appl

c 28	38.2	9.5	1926 6	PCT-US93-07190-22	Sequence 22, Appl
c 29	38.2	9.5	1926 6	PCT-US93-07231-22	Sequence 22, Appl
c 30	38.2	9.5	1926 6	PCT-US93-08742-22	Sequence 22, Appl
c 31	38.2	9.5	1926 6	PCT-US93-08808-22	Sequence 22, Appl
c 32	38.2	9.5	1926 6	PCT-US93-08885-22	Sequence 22, Appl
c 33	38.2	9.5	1926 6	PCT-US93-10520-9	Sequence 9, Appl
c 34	37.4	9.3	806 7	5212286-5	Patent No. 5212286
c 35	34.6	8.7	2589 7	5212286-1	Patent No. 5212286
c 36	34.6	8.6	378 4	US-07-757-606B-2	Sequence 2, Appl
c 37	34.6	8.6	434 4	US-07-757-606B-5	Sequence 5, Appl
c 38	34.6	8.6	549 1	US-07-728-221B-12	Sequence 12, Appl
c 39	34.6	8.6	1020 4	US-07-757-606B-3	Sequence 3, Appl
c 40	34.6	8.6	1020 4	US-07-757-606B-7	Sequence 7, Appl
c 41	34.2	8.5	3252 4	US-08-809-740A-1	Sequence 1, Appl
c 42	34.2	8.5	3252 4	US-08-809-740A-4	Sequence 4, Appl
c 43	33.6	8.4	1313 2	US-08-176-427B-7	Sequence 7, Appl
c 44	33.6	8.4	1313 3	US-08-356-060A-4	Sequence 4, Appl
c 45	33.6	8.4	1843 2	US-08-499-523-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-08-850-910A-44
Sequence 44, Application US/08850910A
Patent No. 5948761
GENERAL INFORMATION:
APPLICANT: SELHAMER, J.J.
APPLICANT: LEWICKI, J.
APPLICANT: SCARBOROUGH, R.M.
TITLE OF INVENTION: RECOMBINANT TECHNIQUES FOR
PRODUCTION OF BRAIN NUTRIENT PEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER, LLP
STREET: 2000 Pennsylvania Avenue, NW, Suite 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850, 910A
FILING DATE: 05-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/477, 226
FILING DATE: 08-FEB-1990
APPLICATION NUMBER: 07/299, 880
FILING DATE: 19-JAN-1989
APPLICATION NUMBER: 07/206, 470
FILING DATE: 14-JUN-1988
APPLICATION NUMBER: 07/200, 383
FILING DATE: 31-MAY-1988
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
REGISTRATION NUMBER: 29, 959
REFERENCE/DOCKET NUMBER: 219002025212
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-867-1500
TELEFAX: 202-822-0168
TELEX:
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 1519 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850,910A
FILING DATE: 05-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/477,226
FILING DATE: 08-FEB-1990
APPLICATION NUMBER: 07/299,880
FILING DATE: 19-JAN-1989
APPLICATION NUMBER: 07/206,470
FILING DATE: 14-JUN-1988
APPLICATION NUMBER: 07/200,383
FILING DATE: 31-MAY-1988
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 219002025212
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEFAX: 202-822-0168
TELEX:
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 1507 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 100...222
OTHER INFORMATION:
NAME/KEY: CDS
LOCATION: 469...723
OTHER INFORMATION:
NAME/KEY: CDS
LOCATION: 1281...1292
OTHER INFORMATION:
US-08-850-910A-38

Query Match 34.6%; Score 139; DB 4; Length 1507;
Best Local Similarity 71.0%; Pred. No. 8.3e-29;
Matches 184; Conservative 0; Mismatches 75; Indels 0; Gaps 0;
QY 130 caggagcagcgcaaccatttcgagggcaaacgtcgagagtcgaggttgagagacatcc 189
DB 466 CAGGAGCTGCTGGAGCGCTCGAGACAGGCTCTCGAGCTCGAGCGGAGCGAGCGAGC 525
QY 190 ctgagagccctccag 249
DB 526 CTGAGAGCCCTCCGCGAGC 585
QY 250 accgagggcattcgtgag 309
DB 586 CCCAGGCGGCTCTGGAGCGCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 645
QY 310 cccaagatggtcgaag 369
DB 646 CCGAAGAGAGATCGTGTACTGTGTGCTTTGGCGAGAGCTGAGCGGAGATCGGCTCCCTC 705
QY 370 agtggccttgagctgcaag 388
DB 706 AGCGGCTGCGCTGCATG 724

RESULT 4
US-08-850-910A-17

Sequence 17, Application US/08850910A
Patent No. 5948761
GENERAL INFORMATION:
APPLICANT: SELHAMER, J.J.
APPLICANT: LEWICKI, J.
APPLICANT: SCARBOROUGH, R.M.
TITLE OF INVENTION: RECOMBINANT TECHNIQUES FOR
TITLE OF INVENTION: PRODUCTION OF BRAIN NUTRIENTIC PEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER, LLP
STREET: 2000 Pennsylvania Avenue, NW, Suite 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850,910A
FILING DATE: 05-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/477,226
FILING DATE: 08-FEB-1990
APPLICATION NUMBER: 07/299,880
FILING DATE: 19-JAN-1989
APPLICATION NUMBER: 07/206,470
FILING DATE: 14-JUN-1988
APPLICATION NUMBER: 07/200,383
FILING DATE: 31-MAY-1988
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 219002025212
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEFAX: 202-822-0168
TELEX:
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1504 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 100...630
OTHER INFORMATION:
US-08-850-910A-17

Query Match 30.8%; Score 123.8; DB 4; Length 1504;
Best Local Similarity 69.9%; Pred. No. 9.8e-25;
Matches 181; Conservative 0; Mismatches 77; Indels 1; Gaps 1;
QY 130 caggagcagcgcaaccatttcgagggcaaacgtcgagagtcgaggttgagagacatcc 189
DB 466 CAGGAGCTGCTGGAGCGCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 524
QY 190 ctgagagccctccag 249
DB 525 CTGAGAGCCCTCCGCGAGC 584
QY 250 accgagggcattcgtgag 309
DB 585 CCCAGGCGGCTCTGGAGCGCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 644
QY 310 cccaagatggtcgaag 369

Dh 645 CCCAGACGATGCTGCTGCTTGGCGAGGCTGACCGATGCTCCCTC 704
QY 370 agtgcctggctgctgcaag 388
Dh 705 AGCGGCTGGGCTGCAATG 723

RESULT 5

US-08-850-910A-42

Sequence 42, Application US/08850910A
Patent No. 5948761
GENERAL INFORMATION:
APPLICANT: SEILHAMER, J.J.
APPLICANT: LEWICKI, J.
APPLICANT: SCARBOROUGH, R.M.
TITLE OF INVENTION: RECOMBINANT TECHNIQUES FOR
TITLE OF INVENTION: PRODUCTION OF BRAIN NUTRIENTIC PEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MORRISON & FOERSTER, LLP
STREET: 2000 Pennsylvania Avenue, NW, Suite 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850,910A
FILING DATE: 05-MAY-1997
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/477,226
FILING DATE: 08-FEB-1990
APPLICATION NUMBER: 07/299,880
FILING DATE: 19-JAN-1989
APPLICATION NUMBER: 07/206,470
FILING DATE: 14-JUN-1988
APPLICATION NUMBER: 07/200,383
FILING DATE: 31-MAY-1988
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 219002025212
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEFAX: 202-822-0168
TELEX:
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 1804 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 365...490
OTHER INFORMATION:
NAME/KEY: CDS
LOCATION: 740...791
OTHER INFORMATION:
NAME/KEY: CDS
LOCATION: 1558...1569
OTHER INFORMATION:
US-08-850-910A-42

Query Match 29.0%; Score 116.4; DB 4; Length 1804;
Best Local Similarity 67.9%; Pred. No. 9.9e-23;
Matches 178; Conservative 0; Mismatches 81; Indels 3; Gaps 1;

QY 127 ttacagagcagcgcaaccattgtgcagggcaaacgtctgagctgaggtggagcagaca 186
Dh 734 ttgcagagactgctgggcccgtctgaaagacgacagtctcagactgcagacagcagtg 793
QY 187 tccctgagagccctccagagagagcccccgtcccaagagtgtctgaaagtcccggaagta 246
Dh 794 gccctggaacccctgcacgagaccacagcccccgcagagaccgccgagagc--gagaga 850
QY 247 gccaccgagggcatcgtgtggcaccgcaaatgtctctctacacccctggggcaccaga 306
Dh 851 agcccccgtggggtccttgcaccccatgacagtgtctcagagccctgaaagactacc 910
QY 307 agcccaagatggtgcaaggtcgtgtctgttgaggaggaagatgaccggtcagctcc 366
Dh 911 agcccaagatgattgcacagtcagaggtcttggccgagagctgacccgattcgctcc 970
QY 367 tccagtgcctggctgctgcaag 388
Dh 971 ctacgtgacctggctgcaatg 992

RESULT 6

US-08-278-729A-22/c

Sequence 22, Application US/08278729A
Patent No. 5650276
GENERAL INFORMATION:
APPLICANT: SMART, JOHN
APPLICANT: OPPERMAN, HERMAN
APPLICANT: OKAMURA, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H. L.
APPLICANT: COHEN, CHARLES M.
TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESSES:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/278,729A
FILING DATE: 20-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER Esq., EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-058CPTW
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 435-9001
TELEFAX: (508) 435-6951
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 1926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 93...1289
OTHER INFORMATION: /Product= "MOP2 CDNA"
US-08-278-729A-22

TELEFAX: (508) 435-6951
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 1926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 93..1289
OTHER INFORMATION: /product= "MOP2 CDNA"
US-08-643-763A-22

Query Match 9.9%; Score 39.8; DB 2; Length 1926;
Best Local Similarity 47.9%; Pred. No. 0.033;
Matches 145; Conservative 0; Mismatches 157; Indels 1; Gaps 1;
66 gggaggtcgtccaccacccgctgggagagcccggttcagccttgagacttgaaagtcg 125
Db 312 gggggcggcagcctgctgctggcggcagccgggttgacagggggtcgggccgtcccg 253
Qy 126 gttaacagagcagcgcacacatttcagagggcaactgtcggagctgcaggttgagcagac 185
Db 252 gttagcccgagcagcccgagatttcacgctgcatgtcgggggcgtcgggccgtccagcc 193
Qy 186 atccctgagccctccagagagcccccgtccacaggtgtctggaagtcccgagag-g 244
Db 192 gacgctggggagacggtgctgggggagcggagcctgctccacggcgagcagag 133
Qy 245 tagccacgagagcgtccgtgggacccgcaaatgtctctacacccctgcggagcaccac 304
Db 132 caagcccaatgacagagtgcccgccggagcagatgcatctcgagactttacggcgccg 73
Qy 305 gaagcccaagatggtgcaaggtgtcgtgctgttgaggagaaagtgaacggatcagct 364
Db 72 gcattcactgtagctgtgctggctgacgacagcgggagagacagacggcgca 13
Qy 365 cct 367
Db 12 cct 10

RESULT 9
US-08-643-763A-22/c
Sequence 22, Application US/08643763A
Patent No. 5733878

GENERAL INFORMATION:
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: OPPERMAN, HERMAN
APPLICANT: COHEN, CHARLES M.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: MORPHOGENIC-INDUCED PERIODONTAL TISSUE
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/643,763A
FILING DATE: 06-MAY-1996
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: FENTON Esq. GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-067CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7560
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 1926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 93..1289
OTHER INFORMATION: /product= "MOP2 CDNA"
US-08-643-763A-22

Query Match 9.9%; Score 39.8; DB 2; Length 1926;
Best Local Similarity 47.9%; Pred. No. 0.033;
Matches 145; Conservative 0; Mismatches 157; Indels 1; Gaps 1;
66 gggaggtcgtccaccacccgctgggagagcccggttcagccttgagacttgaaagtcg 125
Db 312 gggggcggcagcctgctgctggcggcagccgggttgacagggggtcgggccgtcccg 253
Qy 126 gttaacagagcagcgcacacatttcagagggcaactgtcggagctgcaggttgagcagac 185
Db 252 gttagcccgagcagcccgagatttcacgctgcatgtcgggggcgtcgggccgtccagcc 193
Qy 186 atccctgagccctccagagagcccccgtccacaggtgtctggaagtcccgagag-g 244
Db 192 gacgctggggagacggtgctgggggagcggagcctgctccacggcgagcagag 133
Qy 245 tagccacgagagcgtccgtgggacccgcaaatgtctctacacccctgcggagcaccac 304
Db 132 caagcccaatgacagagtgcccgccggagcagatgcatctcgagactttacggcgccg 73
Qy 305 gaagcccaagatggtgcaaggtgtcgtgctgttgaggagaaagtgaacggatcagct 364
Db 72 gcattcactgtagctgtgctggctgacgacagcgggagagacagacggcgca 13
Qy 365 cct 367
Db 12 cct 10

RESULT 10
US-08-462-623-22/c
Sequence 22, Application US/08462623
Patent No. 5739107

GENERAL INFORMATION:
APPLICANT: COHEN, CHARLES M.
APPLICANT: CHARETTE, MARC F.
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: OPPERMAN, HERMAN
APPLICANT: PANG, ROY H.L.
APPLICANT: OKAYNAK, ENGIN
APPLICANT: SMART, JOHN E.
TITLE OF INVENTION: MORPHOGEN TREATMENT OF GASTROINTESTINAL
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748

```
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,623
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/445,882
FILING DATE: 22-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FENTON ESQ., GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-074CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 435-9001
TELEFAX: (508) 435-6951
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 1926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 93..1289
OTHER INFORMATION: /product= "MOP2 CDNA"
US-08-462-623-22
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Query Match          9.9%; Score 39.8; DB 2; Length 1926;
Best Local Similarity 47.9%; Pred. No. 0.033;
Matches 145; Conservative 0; Mismatches 157; Indels 1; Gaps 1;

QY 66 gggaggtgttccaccctgtgagcccggttcagcctcggaattgaaagtcg 125
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 312 gggggcggacgctgctgctccggcgacgctgctgctgctgctgctgctg 253
QY 126 gtaagagagcagcgcaacatttgcagagcaactgtcgagctgcaagtgagagac 185
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 252 gtagcccgagcagccgacgatttgcagctgctgctgctgctgctgctgctg 193
QY 186 atccctgtgagccctccagagagagcccgctcccaagtgctgtaagtcccgagag-g 244
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 192 gacgctggggagacgctgctgggggagcgggacgctgctgctgctgctgctgctg 133
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 245 tagccacgagggcattcgttgggacgcaaatgtctctacacccctgggggacacac 304
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 132 CAAGGCCCAATAGCCAGATGGCCCGGAGCAGCATCTCGGACTTTCAGCCGGCCG 73
QY 305 gaagcccaagatgtgcaaggtgtcgtcttgggaggaagatgagccgagtcagct 364
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 72 GCATCCACTGTGAGCTGTGCTGGGCTGCGTGAAGCCAGCGGGAGAGACCAAGCGCGCA 13
QY 365 cct 367
    |||
DB 12 CCT 10
```

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RESULT 11
US-08-451-953A-22/c
; Sequence 22, Application US/08451953A
; Patent No. 5741641
; GENERAL INFORMATION:
; APPLICANT: SMART, JOHN
; APPLICANT: OPPERMAN, HERMAN
; APPLICANT: OZKAYNAK, ENGIN
; APPLICANT: KUBERASAMPATH, THANGAVEL
; APPLICANT: ROEGER, DAVID C.
; APPLICANT: PANG, ROY H.L.
```

```
APPLICANT: COHEN, CHARLES M.
TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESS: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,953A
FILING DATE: 26-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ., EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-058CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 435-9001
TELEFAX: (508) 435-6951
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 1926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 93..1289
OTHER INFORMATION: /product= "MOP2 CDNA"
US-08-451-953A-22
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Query Match          9.9%; Score 39.8; DB 2; Length 1926;
Best Local Similarity 47.9%; Pred. No. 0.033;
Matches 145; Conservative 0; Mismatches 157; Indels 1; Gaps 1;

QY 66 gggaggtgttccaccctgtgagcccggttcagcctcggaattgaaagtcg 125
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 312 gggggcggacgctgctgctccggcgacgctgctgctgctgctgctgctgctg 253
QY 126 gtaagagagcagcgcaacatttgcagagcaactgtcgagctgcaagtgagagac 185
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 252 gtagcccgagcagccgacgatttgcagctgctgctgctgctgctgctgctgctg 193
QY 186 atccctgtgagccctccagagagagcccgctcccaagtgctgtaagtcccgagag-g 244
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 192 gacgctggggagacgctgctgggggagcgggacgctgctgctgctgctgctgctg 133
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 245 tagccacgagggcattcgttgggacgcaaatgtctctacacccctgggggacac 304
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 132 CAAGGCCCAATAGCCAGATGGCCCGGAGCAGCATCTCGGACTTTCAGCCGGCGC 73
QY 305 gaagcccaagatgtgcaaggtgtcgtcttgggaggaagatgagccgagtcagct 364
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 72 GCATCCACTGTGAGCTGTGCTGGGCTGCGTGAAGCCAGCGGGAGAGACCAAGCGCGCA 13
QY 365 cct 367
    |||
DB 12 CCT 10
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RESULT 12
US-08-445-468A-22/c
; Sequence 22, Application US/08445468A
; Patent No. 5849686
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```

GENERAL INFORMATION:
APPLICANT: KUBERASAMPATH, THANAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: OPPERMAN, HERMAN
APPLICANT: PANG, ROY H.L.
APPLICANT: COHEN, CHARLES M.
TITLE OF INVENTION: MORPHOGEN-INDUCED LIVER REGENERATION
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445,468A
FILING DATE: 22-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: FENTON ESQ., GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-072FW2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7560
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 1926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 93..1289
OTHER INFORMATION: /product= "MOP2 CDNA"
US-08-445-468A-22

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Query Match          9.9%; Score 39.8; DB 3; Length 1926;
Best Local Similarity 47.9%; Pred. No. 0.033;
Matches 145; Conservative 0; Mismatches 157; Indels 1; Gaps 1;

Db 66 ggagaggtcgtcccaaccgctggagagcccggttcagcctcgagacttgaaacgtccg 125
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 312 GGGGCGCGGAGCGTGGCTGGCGGGGAGCGCGGGGTGTGTCACGGGGGTGGGGCGGTCCG 253

Qy 126 gtacagagcagcgcaacattgtcagaggaactgtcgagctgcaggttggagcagac 185
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 252 GTAGCCGAGCAGCGCCAGATTTCAGCTGATGTCGGCGGCGTCCGCCCTCCACAGC 193

Qy 186 atcccttgagccctccagagagcccgctcccaaggtgtctggaaagtccggagag-g 244
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 192 GAGCGTGGGAGCAGGTGTGGCGGGGAGCGGACCGTGGCGCGCTCCAGCGGCACAGAG 133

Qy 245 tagcaccagagagcgtcgtggagcagcgcaaatgtctctacacccctggggagacac 304
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 132 CAAGCCCAATAGCCAGAGTGGCCCGGAGACCATATGCACTTTCAGCCGGGCGC 73

Qy 305 gaagccccaagaatgttgaaaggtctgtgctcttctggaggaagaatggaccgagatcagct 364
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 72 GATCCTCACTGTAGTGTGTCGGGCTGGCTGACGCCAGACGGGAGGAGACAGAGCGCGCA 13

Qy 365 cct 367
    |||
Db 12 CCT 10

```

```

RESULT 13
US-08-461-397A-22/C
Sequence 22, Application US/08461397A
Patent No. 5972884
GENERAL INFORMATION:
APPLICANT: COHEN, CHARLES M.
APPLICANT: CHARETTE, MARC F.
APPLICANT: KUBERASAMPATH, THANAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: OPPERMAN, HERMAN
APPLICANT: PANG, ROY H.L.
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: SMART, JOHN E.
TITLE OF INVENTION: MORPHOGEN TREATMENT FOR LIMITING
PROLIFERATION OF EPITHELIAL CELLS.
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,397A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESQ., EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-074FW2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 1926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 93..1289
OTHER INFORMATION: /product= "MOP2 CDNA"
US-08-461-397A-22

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Query Match          9.9%; Score 39.8; DB 4; Length 1926;
Best Local Similarity 47.9%; Pred. No. 0.033;
Matches 145; Conservative 0; Mismatches 157; Indels 1; Gaps 1;

Db 66 ggagaggtcgtcccaaccgctggagagcccggttcagcctcgagacttgaaacgtccg 125
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Db 312 GGGGCGCGGAGCGTGGCTGGCGGGGAGCGCGGGGTGTGTCACGGGGGTGGGGCGGTCCG 253

Qy 126 gtacagagcagcgcaacattgtcagaggaactgtcgagctgcaggttggagcagac 185
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Db 252 GTAGCCGAGCAGCGCCAGATTTCAGCTGATGTCGGCGGCGTCCGCCCTCCACAGC 193

Qy 186 atcccttgagccctccagagagcccgctcccaaggtgtctggaaagtccggagag-g 244
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Db 192 GAGCGTGGGAGCAGGTGTGGCGGGGAGCGGACCGTGGCGCGCTCCAGCGGCACAGAG 133

Qy 245 tagcaccagagagcgtcgtggagcagcgcaaatgtctctcacccttggggagacac 304
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Db 132 CAAGCCCAATAGCCAGAGTGGCCCGGAGACCATATGCACTTTCAGCCGGGCGC 73

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Best Local Similarity 47.5%; Pred. No. 0.09;
Matches 144; Conservative 0; Mismatches 158; Indels 1; Gaps 1;

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QY 66 gggaggtcgttccaccgctgggcaagcccggtcagcctcggaacttggaaagtcgg 125
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QY 126 gttacagggagcgcaaccatttgcaggcgaactgtcgagctgcaggtgagcagac 185
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Db 252 GTAGCCCGAGACCGCGGATTTCAGGCTGCAATGCGCGCGCTCGCGGCTCCAGGC 193
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QY 186 atccctggaagccctccaggaagcccgctcccaaggtgtctggaagtcgggag-9 244
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Db 192 GACGCTGGGACACAGGTGTGTGGGGAGCGGACCGTGGCCGCTCCAGCGCGCACAGAG 133
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QY 245 tagcaacgagggcatccgttgggcaaccgcaaaatggtcctctaacacctcgggcaaac 304
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    132 CAAGGCCCAATAGCCAGAGTGGCCCGGAGCAGATAGCCATCTCGACTTTCAGCGGCGC 73
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    305 gaagccccaagatggtgcaagggtctggtgtcttgggaagatggaaccggaatcagct 364
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Db 72 GCATCCACTGGTAGTGTGTGGCTCGGCTGACGCCAGACGGGAGGACCAAGCGGCGCA 13
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QY 365 cct 367
    |||
Db 12 Cct 10

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Search completed: April 28, 2000, 00:19:25
Job time: 14557 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 27, 2000, 17:43:46 ; Search time 12.64 Seconds
(without alignments)
140.971 Million cell updates/sec

Title: PEPI
Perfect score: 690
Sequence: 1 mppqtpsrallllllflhla.....rkmdrissssgycvklrrh 134

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 133990 seqs, 13297546 residues

1 number of hits satisfying chosen parameters: 133990

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Issued Patents-AA:*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/PCrUS9_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	690	100.0	134 2 US-08-850-910A-48	Sequence 48, Appl
2	677	98.1	134 2 US-08-850-910A-45	Sequence 45, Appl
3	392	56.8	76 1 US-08-338-358-1	Sequence 1, Appl
4	334.5	48.5	131 2 US-08-850-910A-39	Sequence 39, Appl
5	334.5	48.5	131 2 US-08-850-910A-41	Sequence 41, Appl
6	334.5	48.5	131 2 US-08-850-910A-46	Sequence 46, Appl
7	307	44.5	132 2 US-08-850-910A-47	Sequence 47, Appl
8	289.5	42.0	131 2 US-08-850-910A-43	Sequence 43, Appl
9	202	29.3	106 2 US-08-850-910A-30	Sequence 30, Appl
10	169	24.5	32 1 US-07-828-450-41	Sequence 41, Appl
11	169	24.5	32 1 US-08-297-330-2	Sequence 2, Appl
12	169	24.5	32 1 US-08-451-240-22	Sequence 22, Appl
13	169	24.5	32 2 US-08-470-846A-3	Sequence 3, Appl
14	169	24.5	32 4 PCT-US94-02391-2	Sequence 2, Appl
15	169	24.5	32 4 PCT-US94-12591-22	Sequence 22, Appl
16	158	22.9	32 4 US-08-451-240-3	Sequence 3, Appl
17	158	22.9	32 4 PCT-US94-12591-3	Sequence 3, Appl
18	139	20.1	26 2 US-08-850-910A-1	Sequence 1, Appl
19	122	17.7	32 1 US-07-754-958-5	Sequence 5, Appl
20	122	17.7	32 1 US-07-754-947-5	Sequence 5, Appl
21	113	16.4	125 2 US-08-862-480B-1	Sequence 1, Appl
22	113	16.4	151 5 5212286-2	Sequence 1, Appl
23	108.5	15.7	177 2 US-08-850-910A-18	Sequence 18, Appl
24	106.5	15.4	136 5 5212286-4	Sequence 5, Appl
25	106	15.4	26 1 US-07-778-847-2	Sequence 2, Appl
26	106	15.4	26 2 US-08-850-910A-3	Sequence 3, Appl
27	103.5	15.0	144 5 5202239-1	Sequence 1, Appl
28	103.5	15.0	144 5 5202239-3	Sequence 3, Appl
29	97	14.1	152 5 5212286-6	Sequence 5, Appl

30	92	13.3	29 1 US-07-754-958-6	Sequence 6, Appl
31	29	13.3	29 1 US-07-754-947-6	Sequence 6, Appl
32	87.5	12.7	126 2 US-07-757-606B-1	Sequence 1, Appl
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34	87	12.6	32 1 US-08-451-240-2	Sequence 2, Appl
35	87	12.6	32 1 US-08-737-927-4	Sequence 4, Appl
36	87	12.6	32 2 US-08-470-846A-18	Sequence 18, Appl
37	87	12.6	32 4 PCT-US94-12591-2	Sequence 2, Appl
38	87	12.6	32 5 5449751-1	Sequence 5, Appl
39	87	12.6	32 5 5449751-3	Sequence 5, Appl
40	86	12.5	20 2 US-08-850-910A-34	Sequence 34, Appl
41	82	11.9	22 1 US-07-828-450-10	Sequence 10, Appl
42	82	11.9	22 1 US-07-828-450-13	Sequence 13, Appl
43	82	11.9	27 1 US-07-828-450-5	Sequence 5, Appl
44	82	11.9	27 1 US-08-297-330-4	Sequence 4, Appl
45	82	11.9	27 4 PCT-US94-02391-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-850-910A-48
Sequence 48, Application US/08850910A
Patent No. 5948761
GENERAL INFORMATION:
APPLICANT: SEILAMER, J.J.
APPLICANT: LEWICKI, J.
APPLICANT: SCARBOROUGH, R.M.
TITLE OF INVENTION: RECOMBINANT TECHNIQUES FOR
PRODUCTION OF BRAIN NUTRIENT PEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER, LLP
STREET: 2000 Pennsylvania Avenue, NW, Suite 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850,910A
FILING DATE: 05-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/477,226
FILING DATE: 08-FEB-1990
APPLICATION NUMBER: 07/299,880
FILING DATE: 19-JAN-1989
APPLICATION NUMBER: 07/206,470
FILING DATE: 14-JUN-1988
APPLICATION NUMBER: 07/200,383
FILING DATE: 31-MAY-1988
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 219002025212
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEFAX: 202-822-0168
TELEX:
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 134 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-850-910A-48

[illegible]

US-08-850-910A-45
Sequence 45, Application US/08850910A
Patent No 5948761
GENERAL INFORMATION:
APPLICANT: SELHAMER, J.J.
APPLICANT: LEWICKI, J.
APPLICANT: SCARBOROUGH, R.M.
TITLE OF INVENTION: RECOMBINANT TECHNIQUES FOR
TITLE OF INVENTION: PRODUCTION OF BRAIN NUTRIENT PEPTIDES
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER, LLP
STREET: 2000 Pennsylvania Avenue, NW, Suite 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850,910A
FILING DATE: 05-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/477,226
FILING DATE: 08-FEB-1990
APPLICATION NUMBER: 07/299,880
FILING DATE: 19-JAN-1985
APPLICATION NUMBER: 07/206,470
FILING DATE: 14-JUN-1988
APPLICATION NUMBER: 07/200,383
FILING DATE: 31-MAY-1988
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 219002025212
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEFAX: 202-822-0168
TELEX:
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 134 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: Internal
US-08-850-910A-45

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Query Match 98.1%; Score 677; DB 2; Length 134;
Best Local Similarity 99.3%; Pred. No. 1,4e-69;
Matches 133; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 MDPCAPAPRAL111FLHLAF1GGRSHPLGSGSASD1ETSG1QGRNH1QGRK1SELQVE 60
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OY 61 qtslepi1esprpbv1w1srevategr1rghrkmv1ytl1rapr1spk1mvg1sg1fgr1kmd1 120
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OY 121 ssssg1qcv1lr1rh 134
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1      RESULT      3
2      US-08-338-558-1
3      Sequence 1, Application US/08338558
4      Patent No. 5786163
5      GENERAL INFORMATION:
6      APPLICANT: Hall, Christian
7      TITLE OF INVENTION: BNP ANTIBODY AND IMMUNOASSAY USING ITT
8      NUMBER OF SEQUENCES: 1
9      CORRESPONDENCE ADDRESS:
10     ADDRESSEE: Pennie & Edmonds
11     STREET: 1155 Avenue of the Americas
12     CITY: New York
13     STATE: New York
14     COUNTRY: U.S.A.
15     ZIP: 10036-2711
16
17     COMPUTER READABLE FORM:
18     MEDIUM TYPE: Floppy disk
19     COMPUTER: IBM PC compatible
20     OPERATING SYSTEM: PC-DOS/MS-DOS
21     SOFTWARE: PatentIn Release #1.0, Version #1.30
22
23     CURRENT APPLICATION DATA:
24     APPLICATION NUMBER: US/08/338,558
25     FILING DATE: 21-NOV-1994
26     CLASSIFICATION: 436
27
28     ATTORNEY/AGENT INFORMATION:
29     NAME: Fanucci, Allan A.
30     REGISTRATION NUMBER: 30,256
31     REFERENCE/DOCKET NUMBER: 8080-010
32
33     TELECOMMUNICATION INFORMATION:
34     TELEPHONE: (212) 790-9090
35     TELEFAX: (212) 869-9741/8864
36     TELEX: 66141 PENNIE
37
38     INFORMATION FOR SEQ ID NO: 1:
39     SEQUENCE CHARACTERISTICS:
40     LENGTH: 76 amino acids
41     TYPE: amino acid
42     TOPOLOGY: unknown
43
44     MOLECULE TYPE: protein
45
46     US-08-338-558-1

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Best Local Similarity	100.0%	Pred. No.	1,3e-37			
Matches	76	Conservative	0	Mismatches	0	Indels
						Gaps
						0

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Db	1	hPLGPGSASDLSRSGGLQQRNHLQGLKSLQVETSLDPLQESPRPVGWKSREVAIEG	60
QY	87	lrghrkmlvyltlrapr	102
Db	61	IRGHRKMLVYLTLRAPR	76

US-08-850-910A-45

RESULT 4

Mon May 1 10:09:25 2000

pepl.rai

Page 3

US-08-850-910A-39
Sequence 39, Application US/08850910A
Patent No. 5948761
GENERAL INFORMATION:
APPLICANT: SEILHAMER, J.J.
APPLICANT: LEMICKI, J.
APPLICANT: SCARBOROUGH, R.M.
TITLE OF INVENTION: RECOMBINANT TECHNIQUES FOR
TITLE OF INVENTION: PRODUCTION OF BRAIN NUTRIETIC PEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER, LLP
STREET: 2000 Pennsylvania Avenue, NW, Suite 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850,910A
FILING DATE: 05-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/477,226
FILING DATE: 08-FEB-1990
APPLICATION NUMBER: 07/299,880
FILING DATE: 19-JAN-1989
APPLICATION NUMBER: 07/206,470
FILING DATE: 14-JUN-1988
APPLICATION NUMBER: 07/200,383
FILING DATE: 31-MAY-1988
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 219002025212
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEFAX: 202-822-0168
TELEX:
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-850-910A-39

[illegible]

Sequence 41 Application US/08850910A
Patent No. 5948761

GENERAL INFORMATION:
APPLICANT: SELHAMER, J.J.
APPLICANT: LEWICKI, J.
APPLICANT: SCARBOROUGH, R.M.
TITLE OF INVENTION: RECOMBINANT TECHNIQUES FOR
TITLE OF INVENTION: PRODUCTION OF BRAIN NARIUETIC PEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER, LLP
STREET: 2000 Pennsylvania Avenue, NW, Suite 5500
CITY: Washington
STATE: DC

COUNTRY: USA
ZIP: 20005-1888

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850.910A
FILING DATE: 05-MAY-1997
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/477,226
FILING DATE: 08-FEB-1990
APPLICATION NUMBER: 07/299,880
FILING DATE: 19-JAN-1989
APPLICATION NUMBER: 07/206,470
FILING DATE: 14-JUN-1988
APPLICATION NUMBER: 07/200,383
FILING DATE: 31-MAY-1988

ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 219002025212
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEFAX: 202-822-0168
TELEX:

INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal

US-08-850-910A-41

Query Match	48.5%;	Score 334.5;	DB 2;	Length 131;
Best Local Similarity	53.0%;	Pred. No. 8.9e-31;		
Matches	71;	Conservative	20;	Mismatches 40; Indels 3; Gaps 2;
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		1		
Db	1	MGPRALALRR-VLLLEFLLLLGLGCRSHPGAGALSEL--PEIQLELDLDRURVSELQAE 57		
QY	61	qtsleplqesdprfpgvksrevateg	irghnkmvlytlr	aprspkxmgvsgscifgrkmdti 120
		58		
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QY	121	ssssglqgckvyr	trh 134	
		1		
Db	118	GSLSGLGCNVLRRY 131		
RESULT	6			
US-08-850-910A-46				
Sequence 46, Application	US/08850910A			

Page 4

1 APPLICANT: SEILHAMER, J. J.
 2 APPLICANT: LEWICKI, J.
 3 APPLICANT: SCARBOROUGH, R.M.
 4 TITLE OF INVENTION: RECOMBINANT TECHNIQUES FOR
 5 TITLE OF INVENTION: PRODUCTION OF BRAIN NUTRIENTIC PEPTIDE
 6 NUMBER OF SEQUENCES: 50
 7 CORRESPONDENCE ADDRESSES:
 8 ADDRESSEE: MORRISON & FOERSTER, LLP
 9 STREET: 2000 Pennsylvania Avenue, NW, Suite 5500
 10 City: Washington
 11 STATE: DC
 12 COUNTRY: USA
 13 ZIP: 20006-1888
 14 COMPUTER READABLE FORM:
 15 MEDIUM TYPE: Diskette
 16 COMPUTER: IBM Compatible
 17 OPERATING SYSTEM: Windows
 18 SOFTWARE: FASTED for Windows Version 2.0b
 19 CURRENT APPLICATION DATA:
 20 APPLICATION NUMBER: US/08/850,910A
 21 FILING DATE: 05-MAY-1997
 22 CLASSIFICATION: 435
 23 PRIOR APPLICATION DATA:
 24 APPLICATION NUMBER: 07/477,226
 25 FILING DATE: 08-FEB-1990
 26 APPLICATION NUMBER: 07/299,880
 27 FILING DATE: 19-JAN-1989
 28 APPLICATION NUMBER: 07/206,470
 29 FILING DATE: 14-JUN-1988
 30 APPLICATION NUMBER: 07/200,383
 31 FILING DATE: 31-MAY-1988
 32 ATTORNEY/AGENT INFORMATION:
 33 NAME: Murashige, Kate H
 34 REGISTRATION NUMBER: 29,950
 35 REFERENCE/DOCKET NUMBER: 219002025212
 36 TELECOMMUNICATION INFORMATION:
 37 TELEPHONE: 202-887-1500
 38 TELEFAX: 202-822-0168
 39 TELEX:
 40 INFORMATION FOR SEQ ID NO: 47:
 41 SEQUENCE CHARACTERISTICS:
 42 LENGTH: 132 amino acids
 43 TYPE: amino acid
 44 STRANDEDNESS: single
 45 TOPOLOGY: linear
 46 MOLECULE TYPE: peptide
 47 US-08-850-910A-47

ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1625 L STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/828,450
FILING DATE: 19920131
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: 9437/94133
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3067
TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-828-450-41

Query Match 24.5%; Score 169; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 7.6e-13;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 spkmvgsqcfgrkmdrlsssglgckvllrh 134
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Db 1 SPKMVGSGCFGRKMDRLSSSGLGCKVLLRH 32

RESULT 11
US-08-297-330-2

Sequence 2, Application US/08297330
Patent No. 5583108

GENERAL INFORMATION:

APPLICANT: Wei, Chi-Ming
TITLE OF INVENTION: Vasonaclin Peptide and Analogs
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5583108west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402-4131

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/297,330

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/025,935

FILING DATE: 03-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Woessner, Warren D.

REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 1016.99-US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Mature human brain natriuretic peptide
US-08-297-330-2

Query Match 24.5%; Score 169; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 7.6e-13;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 spkmvgsqcfgrkmdrlsssglgckvllrh 134
|||||
Db 1 SPKMVGSGCFGRKMDRLSSSGLGCKVLLRH 32

RESULT 12
US-08-451-240-22

Sequence 22, Application US/08451240
Patent No. 5665704

GENERAL INFORMATION:

APPLICANT: Lowe, David
APPLICANT: Cunningham, Brian
APPLICANT: Oare, David
APPLICANT: McDowell, Robert S.
TITLE OF INVENTION: RECEPTOR SPECIFIC ATRIAL NATRIURETIC
TITLE OF INVENTION: PEPTIDES
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,240

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/362552

FILING DATE: 06-JAN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/152994

FILING DATE: 12-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: Kudinec, Jeffrey S.

REGISTRATION NUMBER: 36,575

REFERENCE/DOCKET NUMBER: P0844P1C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-8228

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids

TYPE: amino acid
TOPOLOGY: linear
US-08-451-240-22

Query Match 24.5%; Score 169; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 7.6e-13;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 spkmvqsgcfcgrkmdrissssglgckvllrrh 134
|||||
DB 1 SPKMVQSGCFCGRKMDRISSSSGLGCKVLLRRH 32

RESULT 13
US-08-470-846A-3

Sequence 3, Application US/08470846A
Patent No. 5846932

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

APPLICANT: Lowe, David G.

APPLICANT: Cunningham, Brian C.

APPLICANT: Oare, David

APPLICANT: McDowell, Robert S.

TITLE OF INVENTION: RECEPTOR SPECIFIC ATRIAL NATRIURETIC PEPTIDES

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Minipath (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/470,846A

FILING DATE: 06-Jun-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/419877

FILING DATE: 11-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/362552

FILING DATE: 06-JAN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/152994

FILING DATE: 12-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: Rubinec, Jeffrey S.

REGISTRATION NUMBER: 36,575

REFERENCE/DOCKET NUMBER: P0844P2C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-8228

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 32 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-08-470-846A-3

Query Match 24.5%; Score 169; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 7.6e-13;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 103 spkmvqsgcfcgrkmdrissssglgckvllrrh 134

DB 1 SPKMVQSGCFCGRKMDRISSSSGLGCKVLLRRH 32
|||||

RESULT 14
PCT-US94-02391-2

Sequence 2, Application PC/TUS9402391

GENERAL INFORMATION:

APPLICANT: Mayo Foundation for Medical Education and Research

APPLICANT: 200 First Street S.W. 55905 USA

APPLICANT: Rochester, Minnesota

TITLE OF INVENTION: Vasopressin Peptide and Analogs Thereof

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Schwegman, Lundberg & Woessner

STREET: 3500 IDS Center

CITY: Minneapolis

STATE: MN

COUNTRY: USA

ZIP: 55402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/02391

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/025,935

FILING DATE: 03-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Woessner, Warren D.

REGISTRATION NUMBER: 30,440

REFERENCE/DOCKET NUMBER: 150.99US01

TELECOMMUNICATION INFORMATION:

TELEPHONE: 612-339-3061

TELEFAX: 612-339-3061

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 32 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

PCT-US94-02391-2

Query Match 24.5%; Score 169; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 7.6e-13;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 spkmvqsgcfcgrkmdrissssglgckvllrrh 134
|||||
DB 1 SPKMVQSGCFCGRKMDRISSSSGLGCKVLLRRH 32

RESULT 15
PCT-US94-12591-22

Sequence 22, Application PC/TUS9412591

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

APPLICANT: Cunningham, Brian C.

APPLICANT: Oare, David

APPLICANT: McDowell, Robert S.

TITLE OF INVENTION: RECEPTOR SPECIFIC ATRIAL NATRIURETIC

PEPTIDES

NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: patin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/12591
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/152994
 FILING DATE: 12-NOV-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Winter, Daryl B.
 REGISTRATION NUMBER: 32,637
 REFERENCE/DOCKET NUMBER: 844P1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-1249
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 32 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 PCT-US94-12591-22

Query Match 24.5%; Score 169; DB 4; Length 32;
 Best Local Similarity 100.0%; Pred. No. 7 6e-13;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 103 spkmvgsqgcfgrkmdrissssg1gckv1rrh 134
 Db 1 spkmvgsqgcfgrkmdrissssg1gckv1rrh 32

Search completed: April 27, 2000, 18:34:45
 Job time: 3059 sec


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RT      "Cloning of an unusual natriuretic peptide from the South American
KT      coral snake Micrurus corallinus." ;
RL      Eur. J. Biochem. 250:144-149(1997).
DR      EMBL: U77596; AAC60341.1; -
DR      PROSITE; PS00263; NATRIURETIC_PEPTIDE; 1.
DR      PFAM; PF00212; ANP; 1.
DR      PRINTS; PR00710; NATPEPTIDES.
SQ      SEQUENCE 139 AA; 14881 MW; 05421ABB CRC32;

      Query Match      13.1%; Score 90.5; DB 13; Length 139;
      Best Local Similarity 31.9%; Pred. No. 0.064;
      Matches 23; Conservative 9; Mismatches 25; Indels 15; Gaps 2;

Qy      61 qtsleplqesprtgwksrevategirghrkmylrlraprpskmvgsgcfrkmdri 120
      | : : | | | : | : | | | | | | | | | | | | | | | |
Db      50 QAVLDPMVHPERAG-----SGDGDGR-----RLEGLAKEALGDGCFQRI 94

Qy      121 ssssglgckvlr 132
      : | | : | |
Db      95 CNVSGMGCNHVR 106

RESULT 8
Q9Y2Y4
ID      Q9Y2Y4 PRELIMINARY; PRT; 487 AA.
AC      Q9Y2Y4;
DT      01-NOV-1999 (TEMBLrel. 12, Created)
DT      01-NOV-1999 (TEMBLrel. 12, Last sequence update)
DT      01-NOV-1999 (TEMBLrel. 12, Last annotation update)

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DE TESTIS ZINC FINGER PROTEIN.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-TESTIS;
RA TANG T.K., LAI C.-H., TANG C.-J., HUANG C.-J., LIN W.-C.;
RT "Identification and gene structure of a novel human PLZF related
RT transcription factor gene, TZFP."
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF130255; AAD27708.1; -.
SQ SEQUENCE 487 AA; 52962 MW; E3F0D6BF CRC32;

Query Match 12.4%; Score 85.5; DB 4; Length 487;
Best Local Similarity 25.2%; Pred. No. 0.81;
Matches 33; Conservative 24; Mismatches 55; Indels 19; Gaps 5;

QY* 18 hlaflgrshplspgs---asdlsglqeqnrlhlgklselqveqtsleplqesprpt 74
DB 43 HSLVLGVQQLRRGQWALGEGISPTFAQLNLFVYGESVELQPGF--LRPLQEAARAL 100
QY 75 qv-----wksr-----evateglgrkmvlytlrapspkmvggscfgrkmdriss 123
DB 101 GVOSLEACHWRAGDRAKKPDGLKKHQE---BPEKPSRPERELGDPGEKQPEQVSR 157
QY 124 sglgckvlrrh 134
DB 158 GGREQEMLHKH 168

RESULT 9
O70373 PRELIMINARY; PRT; 1677 AA.
AC O70373
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE XIN.
GN XIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-CARDIAC MUSCLE;
RA WANG D.-Z., HU X., LIN J.L.-C., KITTEN G.T., SOLURSH M., LIN J.J.-C.;
RL Front. Biosci. 1:0-0(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-CARDIAC MUSCLE;
RA WANG D.-Z., LIN J.J.-C.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF051945; AAC06023.1; -.
DR MGD: MGI:1333878; Xin.
SQ SEQUENCE 1677 AA; 182085 MW; 106A30FA CRC32;

Query Match 11.8%; Score 81.5; DB 11; Length 1677;
Best Local Similarity 25.8%; Pred. No. 8;
Matches 24; Conservative 15; Mismatches 35; Indels 19; Gaps 2;

QY 47 rnhlqgklselqveqtsleplqesprptgwkrevateg-----irg 89
DB 109 RGLPLGNLCQVATSRPPLSLKAPLPTAIRSRRTSRSGDVQAAQMPETKPLDALRG 168
QY 90 hrkmvlytlrapspkmvggscf--grkmdri 120
DB 169 QEATQTTREPATGDVQGTAKLFETPLDRL 201

RESULT 10

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O82861 PRELIMINARY; PRT; 1326 AA.
AC O82861
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE CELLULOSE SYNTHASE SUBUNIT C.
GN BCSC.
OS Acetobacter xylinum (Acetobacter pasteurianus).
OC Bacteria; Proteobacteria; alpha subdivision; Acetobacteraceae;
OC Acetobacter.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BPR2001;
RA UMEYAMA T., TONOUCHI N.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BPR2001;
RX MEDLINE: 98296257.
RA NAKAI T., MORIYA A., TONOUCHI N., TSUCHIDA T., YOSHINAGA F.,
RA HORINOCHI S., SONE Y., MORI H., SAKAI F., HAYASHI T.;
RT "Control of expression by the cellulose synthase (bcsA) promoter
RT region from Acetobacter xylinum BPR 2001."
RL Gene 213:93-100(1998).
DR EMBL: AB010645; BAA31465.1; -.
SQ SEQUENCE 1326 AA; 142103 MW; F49C1753 CRC32;

Query Match 11.4%; Score 78.5; DB 2; Length 1326;
Best Local Similarity 24.0%; Pred. No. 12;
Matches 29; Conservative 19; Mismatches 50; Indels 23; Gaps 4;

QY 2 dpq-tapsrallllflhlaflgrshplspgsasdlsglqeqnrlhlgklselqve 50
DB 731 DPEATSPKLALRYNGH-----GKPKALEIDLAVLRHNPQDLDAQAQVAA 779
QY 61 qts-----leplqesprptgwkrevateglgrkmvlytlrapspkmvggs 110
DB 780 VNSNHNLSATRLAMDGVQSPMDARWLAMAVADQA-DGHGQRTIEDLRAYDLRLQOYE 838
QY 111 g 111
DB 839 G 839

RESULT 11
Q28644 PRELIMINARY; PRT; 1984 AA.
AC Q28644
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE SODIUM CHANNEL ALPHA-SUBUNIT.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NEW ZEALAND WHITE; TISSUE-SCIATIC NERVE;
RX MEDLINE: 96074641.
RA BELCHER S.M., ZERILLO C.A., LEVENSON R., RITCHIE J.M., HOWE J.R.;
RT "Cloning of a sodium channel alpha subunit from rabbit Schwann
RT cells."
RL Proc. Natl. Acad. Sci. U.S.A. 92:11034-11038(1995).
DR EMBL: U35238; AAA89159.1; -.
DR PFAM: PF00520; Ion_trans; 4.
DR PFAM: PF00612; IQ; 1.
DR PRINTS: PR00170; NACHANNEL.
KW Ionic channel.
SQ SEQUENCE 1984 AA; 225748 MW; EF89D962 CRC32;

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Query Match          10.9%; Score 75.5; DB 12; Length 780;
Best Local Similarity 27.4%; Pred. No. 14;
Matches 29; Conservative 13; Mismatches 47; Indels 17; Gaps 3;

QY 12 lllflblhaf--lgrshbplgspgsasdlsetsglqeqrnhihgkklseiqvetslepiqe 69
   : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 680 ILRLFFKCAENMTLSASKPRYPGKAYNNLR-----KNDLENLMDNWEISRTNLKTCKE 733
   : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 70 spcptgwksrevateglgrhkmvlytlraprsgkmvgsgscfgr 115
   : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 734 -----LRKALTEASRRARKOTIYKLGQSDISLSVSEVGVFGQ 770
   : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 13
Q921P7      PRELIMINARY;          PRT;      791 AA.
ID   Q921P7
AC   Q921P7; 10-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   N28.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Mammalia;
OC   Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129;
RC   ROWEN L., QIN S., MADAN A., LORETZ C., HALL J., JAMES R., DORS M.,
RC   SHAFFER T., ABBASI N., RATCLIFFE A., DICKHOFF R., LASKY S., HOOD L.;
RT   "Sequence of the mouse major histocompatibility complex class II
RT   region.";
RL   Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR   EMBL; AF110520; AAC97966.1; -.
DR   HSSP; P42773; 1B09.
SQ   SEQUENCE 791 AA; 84186 MW; 495A3736 CRC32;

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Query Match          10.8%; Score 74.5; DB 2; Length 418;
Best Local Similarity 24.5%; Pred. NO. 8.7;
Matches 38; Conservative 10; Mismatches 42; Indels 65; Gaps

Qy      7 psrallllflfhlafl-----ggrshplsgpsasdlsetglgeqrnhlgkkl 54
         ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      224 PTRRRLLAGLQLSEHAPANGRLADTPRGHRPHP-AMP-----QRPLRRQR---QTPL 273
                                         :||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      55 selqveqtsleqlgesp-----rptgvwvksr 80
         ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      274 PLVQMRODLEFLPQQPPVDLAHNHPAPTATRLKQNTMLLPYSHSFGSVATRPGW--R 331
                                         ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      81 evategirghrmkvlytlraprspkmvgsgcfr 115
         .||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      332 RSPTRGRARR-----RSPTAPRTNRRGPATGR 359
                                         ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 15
ID1212 PRELIMINARY; PRT; 557 AA.
AC O18212
DT DT 01-JAN-1998 (TREMblrel. 05, Created)
DT DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DE DE 01-JAN-1999 (TREMblrel. 09, Last annotation update)
GN Y53C12A.3 PROTEIN.
OS Y53C12A.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditiia; Rhabditida;
OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
[1]
RN RP SEQUENCE FROM N.A.
RA KERSHAW J.; LENNARD N.;
```

```

Query Match          10.8%; Score 74.5; DB 2; Length 418;
Best Local Similarity 24.5%; Pred. NO. 8.7;
Matches 38; Conservative 10; Mismatches 42; Indels 65; Gaps

Qy      7 p s r a l l i l f h l a f l ----- g r s p l g s p g s a d l e t s g l g c e q r n h l g k l 54
       | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      224 P T R R R L L A G L Q L S H A P A N R G L A D T D R G H R P H P - A M P ----- Q R P L R R Q R --- O T P L 273
       | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy     55 s e l g v e q t s l e p l g e s p ----- r t p g v w k s r 80
       | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     274 P L V Q M R Q D L E P L Q P P V D L A H N E P T A P T R L K Q N T M L L P Y S H S A F G S V A T R P A G W - R 331
       | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy     81 e v a t e g i r g h k m v l y t l r a p s p k m v g s g c f g r 115
       | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    332 R S P T R G R R A R R ----- R S P T A P T R N G R R P A T G R 359
       | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 15
ID1212 PRELIMINARY; PRT; 557 AA.
AC O18212
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DE 01-JAN-1999 (TREMBlrel. 09, Last annotation update)
DE Y53C12A.3 PROTEIN.
GN Y53C12A.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditiia; Rhabditida;
OC Rhabditiina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
[1]
RN SEQUENCE FROM N.A.
RP KERSHAW J., LENNARD N.;
```

```

Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
[2]
RL  SEQUENCE FROM N.A.
RN  MEDLINE: 94150718.
RP  WILSON R., AINSOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RX  BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA  CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FUTON L.,
RA  GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA  JONES M., KESHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA  LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA  PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA  SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA  THERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA  WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT  *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RL  elegans.*;
RL  Nature 368:32-38(1994).
DR  EMBL: 299277; CAB16487.1; -.
SQ  SEQUENCE 557 AA; 63505 MW; 228F96B1 CRC32;

Query Match      10.8%; Score 74.5; DB 5; Length 557;
Best Local Similarity 21.2%; Pred. No. 12;
Matches 32; Conservative 26; Mismatches 50; Indels 43; Gaps 6;

QY  11 lllllflhlafl---lgrsrhplgpgsaadletsqleq-----rnhlq--- 52
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Db  263 LLLIIILYLFHGFVHVEELEDEVMGD-----AIVDVNAIKETLPISFIKFSEHVLNIFYDII 318
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|

QY  52 -----gklselqveqtsleqlpsprtgvgwksrevategirghrkmvlytlrapr--- 103
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Db  319 YRVPMVSIVEHQVQLVSEDPDPIENCVKST-----CPGCKSNRRKIFYCDTCDTPMGVF 369
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Search completed: April 27, 2000, 21:53:26
Job time: 12287 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 27, 2000, 20:11:09 ; Search time 386.23 Seconds
(without alignments)
-3160.361 Million cell updates/sec

Title: SEQ1
Perfect score: 402
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 821193 seqs, -1518192014 residues
Total number of hits satisfying chosen parameters: 1642386
Minimum DB seq length: 0
Maximum DB seq length: 1000000
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : GenEmbl.*

1: gb_ba1.*
2: gb_ba2.*
3: gb_ov.*
4: gb_ov.*
5: gb_pat.*
6: gb_pat.*
7: gb_pl1.*
8: gb_pl2.*
9: gb_pr1.*
10: gb_pr2.*
11: gb_pr3.*
12: gb_ro.*
13: gb_sts.*
14: gb_sy.*
15: gb_un.*
16: gb_v1.*
17: em_fun.*
18: em_hum1.*
19: em_hum2.*
20: em_in.*
21: em_om.*
22: em_or.*
23: em_ov.*
24: em_pat.*
25: em_ph.*
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27: em_ro.*
28: em_sts.*
29: em_sy.*
30: em_un.*
31: em_v1.*
32: gb_htg1.*
33: gb_htg2.*
34: gb_in1.*
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36: em_ba1.*
37: em_ba2.*
38: em_hum3.*
39: em_hum4.*
40: gb_pr4.*
41: gb_htg3.*
42: gb_htg4.*
43: gb_htg5.*
44: gb_htg6.*

45: gb_htg7.*
46: em_htg1.*
47: em_htg2.*
48: em_htg3.*
49: em_hum5.*
50: gb_pl3.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	402	100.0	692	5	E02602
2	402	100.0	692	9	HUMNATPEP
3	320.8	79.8	888	5	E04396
4	320.8	79.8	888	5	E04396
5	260.4	64.8	1922	9	HUMNPA
6	260.4	64.8	107603	11	HS934G17
7	180.6	44.9	669	5	E02365
8	180.6	44.9	670	3	P1GBNP
9	165	41.0	732	5	E04397
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11	139	34.6	1479	3	P1GBNPA
12	132.4	32.9	331	13	G09534
13	120.4	30.0	2125	3	AF037466
14	116.4	29.0	1803	3	DOGNPA
15	96	23.9	96	5	E05300
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17	81.2	20.2	603	12	HAMBNPB
18	60.2	15.0	628	5	E02718
19	60.2	15.0	628	12	RATBNP
20	53.8	13.4	1301	12	RATISOANP
21	53.8	13.4	2575	12	RATISO
22	52.4	13.0	755	4	GGNATRIUP
23	52.4	13.0	755	5	E02222
24	52	12.9	96	5	E05301
25	51	12.7	828	5	E07271
26	51	12.7	831	5	E07269
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ALIGNMENTS

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DEFINITION DNA encoding human brain natriuretic peptide(human BNP).
ACCESSION E02602
VERSION E02602.1
KEYWORDS JP 1990231082-A/1.

29-SEP-1997

RESULT 3
 LOCUS E04396 888 bp RNA PAT 29-SEP-1997
 DEFINITION DNA sequence encoding human brain natriuretic peptide.
 ACCESSION E04396
 VERSION E04396.1 GI:2172597
 KEYWORDS JP 1993056794-A/1.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 888)
 AUTHORS Mori, T., Maekawa, K., Izumi, A. and Sudo, T.
 TITLE PRODUCTION OF PHYSIOLOGICALLY ACTIVE PEPTIDE
 JOURNAL Patent: JP 1993056794-A 1 09-MAR-1993;
 DAI ICHI PURE CHEM CO LTD, DAI ICHI SEIYAKU CO LTD
 COMMENT OS Homo sapiens (human)
 PN JP 1993056794-A/1
 PD 09-MAR-1993
 PF 03-SEP-1991 JP 1991222783
 PI MORI TOKUO, MAEKAWA KEIJI, IZUMI ATSUSHI, SUDO TETSUJI PC
 C12P21/02, C12N15/62, C12N15/70//A61K37/02, A61K37/02, A61K37/02, PC
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 CC topology: Linear;
 CC hypothetical: No;
 CC anti-sense: No;
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 DEFINITION DNA encoding recombinant hBNP(human Brain Natriuretic Peptide).
 ACCESSION E04438
 VERSION E04438.1 GI:2172639

KEYWORDS JP 1993068581-A/1.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 888)
 AUTHORS Mori, T., Maekawa, K., Izumi, A. and Sudo, T.
 TITLE PRODUCTION OF PHYSIOLOGICALLY ACTIVE PEPTIDE
 JOURNAL Patent: JP 1993068581-A 1 23-MAR-1993;
 DAI ICHI PURE CHEM CO LTD, DAI ICHI SEIYAKU CO LTD
 COMMENT OS Homo sapiens (human)
 PN JP 1993068581-A/1
 PD 23-MAR-1993
 PF 10-SEP-1991 JP 1991230597
 PI MORI TOKUO, MAEKAWA KEIJI, IZUMI ATSUSHI, SUDO TETSUJI PC
 C12P21/02, C12N15/62//A61K37/02, A61K37/02, A61K37/02, C07K7/10, PC
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 Matches 322; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 79 caccctgggagcccccgttcagctcgacttgaaactgcgggttacaggagcag 138
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 Db 766 GGCTGCAAGTGTGAGGGCGCAT 789
 RESULT 5
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 DEFINITION Human brain natriuretic protein (BNP) gene, complete cds.
 ACCESSION M31776
 VERSION M31776.1 GI:179514
 KEYWORDS brain natriuretic protein; protein hormone.
 SOURCE Human DNA, clone H1.
 ORGANISM Homo sapiens

ACCESSION	STSS and the genomic marker D1S2740, complete sequence.
AL021155	
VERSION	AL021155.1 GI:3171888
KEYWORDS	HTG; ANF; ANP; Atrial Natriuretic Factor; Atrial Natriuretic peptide; BNP; Brain Natriuretic Protein; chloride channel; CLC-6; CLCN6; D1S2740; KIAA0046; Myotubularin-related protein; NPPA; SBFI. human.
SOURCE	
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 107603)
TITLE	Errington,H.
JOURNAL	Direct Submission
COMMENT	Submitted (12-MAY-1998), Chromosome 1 Project Group (http://www.sanger.ac.uk/HGP/Chrl/) Sanger Centre, Cambridgehire, CB10 1SA, UK. E-mail enquires: humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jun 2, 1998 this sequence version replaced gi:2769553. IMPORTANT: This sequence is the entire insert of clone 934G17. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variations annotated may not be found in the sequence submission corresponding to the overlapping clone as we submit sequences with only a small overlap as described above. This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre chromosome 1 mapping group. Further information can be found at http://www.sanger.ac.uk/HGP/Chrl/ This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known, annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The true left end of clone 934G17 is at 1 in this sequence. The true right end of clone 934G17 is at 107603. 934G17 is from the library RPC15 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ .

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RESULT	10
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DEFINITION	DNA encoding recombinant hBNP(human Brain Natriuretic Peptide)
ACCESSION	E04439
VERSION	E04439.1 GI:2172640
KEYWORDS	JP 1993068581-A/2.
SOURCE	Homo sapiens.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
AUTHORS	Primates; Catarrhini; Hominidae; Homo.
TITLE	1 (bases 1 to 732)
JOURNAL	Mori,T., Maekawa,K., Izumi,A. and Sudo,T.. PRODUCTION OF PHYSIOLOGICALLY ACTIVE PEPTIDE Patent: JP 1993068581-A 2 23-MAR-1993; DAI ICHI PURE CHEM CO LTD, DAI ICHI SEIYAKU CO LTD
COMMENT	OS Homo sapiens (human) PN JP 1993068581-A/2 PD 23-MAR-1993 PF 10-SEP-1991 JP 1991230597 PI MORI TOKUO, MAEKAWA KEIJI, IZUMI ATSUSHI, SUDO TETSUJI PC C12P21/02.C12N15/62//A61K37/02.A61K37/02.C07K7/10.PC (C12P21/02. PC C12R1.19).C07K99:00; CC strandedness: Double; CC topology: Linear; CC hypothetical: No; CC anti-sense: No; CC *source: clone-pKKrIbB; FH Key Location/Qualifiers FT misc_feature 1..732 FT /note-'DNA encoding recombinant hBNP'.
FEATURES	Location/Qualifiers 1..732 /organism='Homo sapiens' /db_xref='taxon:9606'
BASE COUNT	204 a 180 c 174 g 174 t
ORIGIN	
Query Match	41.0%; Score 165; DB 5; Length 732;
Best Local Similarity	85.9%; Pred.No. 7.6e-32;
Matches 183; Conservative	0; Mismatches 30; Indels 0; Gaps
Qy 190	ctggagccctccaggagacccccgccaggtgctcgaagtcccgcggagtagcc 249
Db 421	CAGGTGCACCTGCGACGGGACTGCCCTCCATCATAGATTTCAGATCGGGAGTAGCC 480
Qy 250	accgagggcatccgtgggcacgcgcaaaatggtctctctataccctcgggcacccagaagc 309
Db 481	ACCGAGGGCATCGCTGGGCACCGCAAATGGTCTCTACACCCTCGGGGCACACGAGAC 540
Qy 310	cccaaatgctcaagggtctgctcttggaggaagatgacccgatcagctccctcc 369
Db 541	CCCAAGAIGTGCAAGGGTCTGGCTCTTTGGAGGAAGATGACCGGATCAGCTCCTCC 600
Qy 370	agtggcctgggtgcgaagtgtctgagcggcat 402
Db 601	AGTGCCCTGGGCTGCAAAAGTGCTGAGCGGCAT 633
RESULT	11
P1GBNPA	
LOCUS	1479 bp DNA MAM 27-APR-1993
DEFINITION	pig brain natriuretic peptide (BNP) mRNA, complete cds.
ACCESSION	M25547 J04708 M22477 M22478
VERSION	M25547.1 GI:164392
KEYWORDS	brain natriuretic peptide.
SOURCE	Pig atrium RNA, and cDNA to mRNA, clones 14b, 15a.
ORGANISM	Sus scrofa

```

REFERENCE 1 Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
AUTHORS Porter, J.G., Arfsten, A.E., Palisi, T., Scarborough, R.M.,
         Lewis, J.A., and Sellhammer, J.J.
TITLE Cloning of a cDNA encoding porcine brain natriuretic peptide
JOURNAL J. Biol. Chem. 264, 6689-6692 (1989)
MEDLINE 89214071
COMMENT Draft entry and computer-readable sequence [1] kindly submitted by
         J.J. Sellhammer, 09-FEB-1989.
FEATURES   source      location/Qualifiers
           1..1479
           /organism="Sus scrofa"
           /db_xref="taxon:9823"
           /tissue_type="atrium"
           <1..218
           /gene="BNP"
           /number=1
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           /gene="BNP"
           94..162
           /gene="BNP"
           join(94..216,463..718,1273..1289)
           /gene="BNP"
           /codon_start=1
           /product="brain natriuretic peptide"
           /protein_id="AAA31007.1"
           /db_xref="GI:164393"
           /translation="MGRPALPRVLLLFHLLLCRSHPLGAGLASELPQIQELL
DRLDVRVSEIQAEITDLEPLRQGLTEAWEARAAPTGLVGRSSIFQVLRIRSPK
TMRDSCGFGRRLDRIQSLGSLGCVLRY"
           217..462
           /gene="BNP"
           /number=1
           463..718
           /gene="BNP"
           /number=2
           719..1272
           /gene="BNP"
           /number=2
           303 a 448 c 404 g 324 t
           /number=2
BASE COUNT 303 a 448 c 404 g 324 t
ORIGIN
Query Match 34.68; Score 139; DB 3; Length 1479;
Best Local Similarity 71.08; Pred. No. 2.5e-25;
Matches 184; Conservative 0; Mismatches 75; Indels 0; Gaps 0;
QY 130 caggagcagcgaaccatttcagggaacaaactgcgagctgcaggtgagcagacatcc 189
Db 460 CAGGAGCTGCTGGACCGCTCCGAGACAGAGGTCTCCGAGCTGCAGGCGGAGCGGAC 519
QY 190 ctggagccctccaggagagcccgctccacaggtgtctggaagtcccgaggtagcc 249
Db 520 CTGGAGCCCTCCGAGGACCGGTGGCTCAGAGAGCTGGAGGAGGAGGAGGAGGAGCC 579
QY 250 accagggcctccgtgggacccgcaaaatggtctctacacccctgcgggacccagc 309
Db 580 CCCACGGGGGTCTTGGGCGCCGAGTAGCATCTTCCAAAGTCCCTCCGGGAATACGAGC 639
QY 310 cccaagatggtgcaaggtctggtcttggaggaagatggaccgagatcagctctcc 369
Db 640 CCCAAGACATGCGTACTCTGGTCTGCTTTGGCGGAGGCTGGACCGATCGGCTCCTC 699
QY 370 agtggcctgggctgcaag 388
Db 700 AGCGGCTGGGCTGCAATG 718
RESULT. 12
G09534

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LOCUS      G09534          331 bp      DNA          STS          15-AUG-1995
DEFINITION human STS CHLC.GCT3H01.P11079 clone GCT3H01.
ACCESSION  G09534
VERSION    G09534.1  GI:941383
KEYWORDS   STS sequence; primer; sequence tagged site.
SOURCE     human vector-pjCPI host-E.coli dut+ung+ (DH10B) Marker Selected
           genomic DNA prepared from xy individual of French nationality.
ORGANISM   Homo sapiens
           Eukaryotae; mitochondria; eukaryotes; Metazoa; Chordata;
           Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata;
           Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
           Catarrhini; Hominoidea; Homo.
REFERENCE  1 (bases 1 to 331)
AUTHORS   Murray, J., Sheffield, V., Weber, J.L., Duyk, G. and Buetow, K.H.
TITLE     Cooperative Human Linkage Center
JOURNAL   Unpublished (1995)
COMMENT    Synonyms: GCT3H01, CHLC.GCT3H01.T11078
           Contact: Dr. Jeffrey C. Murray
           UofI
           The University of Iowa
           Department of Pediatrics, Iowa City, IA 52242, USA
           Tel: (319) 356-3508
           Fax: (319) 356-3347
           Email: jeff-murray@uiowa.edu
PRIMER A: AGGAGCCAGGAGGAGGAC
PRIMER B: ATCCATGCTCTCGAGGAC
STS SIZE: 124
PCR PROFILE:
denature: 30 seconds at 94 degrees C
annealing: 75 seconds at 55 degrees C
extension: 15 seconds at 72 degrees C
PCR cycles: 27
extension: 6 minutes at 72 degrees C
Protocol:
Template: 30ng genomic DNA
Primer: each 1.5 pmole
dNTPs: each 200 uM
Tag Polymerase: 0.3 units
Total Vol: 10 ul
Buffer:
MgCl2: 1.5mM
KCl: 50mM
Tris: 10mM
pH: 8.3
FEATURES   Location/Qualifiers
           source      1..331
           STS         /organism="Homo sapiens"
           primer_bind 12..135
           primer_bind 12..29
           BASE COUNT 68 a 104 c 106 g 50 t 3 others
ORIGIN
Query Match 32.9%; Score 132.4; DB 13; Length 331;
Best Local Similarity 98.5%; Pred. No. 1.3e-23;
Matches 133; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 atggatccccagacagcaccttcccgggcgctcctgctcctcttcttgcattcggt 60
Db 130 ATGATCCCCAGACAGACACCTTCCGCGGCTCTCTCTCTCTCTCTCTCTCTCTCT 189
QY 61 ttctctgggaggttgcttccacacccgctggcgagcccggttcagctcggactggaaag 120
Db 190 TTCCTGGAGGTCGTCCACCGCTGGGAGCCCGGTTTCAGCTCGGACTTGGAAACG 249
QY 121 tccgggttacaggag 135
Db 250 TCCGGGTACAGGTG 264

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RESULT 13
AF037466
LOCUS
DEFINITION
Ovis aries brain natriuretic peptide (BNP) gene, complete cds.
ACCESSION
AF037466
VERSION
AF037466.1 GI:2708651
KEYWORDS
sheep.
SOURCE
ORGANISM
Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Ovis.
REFERENCE
1 (bases 1 to 2125)
Aitken, G.D., Raizis, A.M., George, P.M., Espiner, E.A. and
Cameron, V.A.
TITLE
The Characterization of Ovine Genes for Atrial, Brain and C-Type
Natriuretic Peptides
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 2125)
Aitken, G.D., Raizis, A.M., George, P.M., Espiner, E.A. and
Cameron, V.A.
AUTHORS
Direct Submission
TITLE
Submitted (08-DEC-1997) Medicine, University of Otago, Riccarton
JOURNAL
Ave, Christchurch, Canterbury, New Zealand
FEATURES
Location/Qualifiers
1..2125
/organism="Ovis aries"
/db_xref="taxon:9940"
join(<870..995,1274..1520,2054..>2070)
/gene="BNP"
/product="brain natriuretic peptide"
<870..>2070
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join(870..995,1274..1520,2054..>2070)
/gene="BNP"
/codon_start=1
/product="brain natriuretic peptide"
/protein_id="AAB92565.1"
/db_xref="GI:2708652"
/translation="MDPKALSRLLLLFLHLSLGLGRSHPLGPGGSASELPGLQEL
LDRLDRVSELQAEOLRVEPLQGGGLEETWDSRAAPAGFLGPHHSLQLALRGFKM
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-BASE COUNT 431 a 654 c 648 g 392 t
ORIGIN

Query Match 30.0%; Score 120.4; DB 3; Length 2125;
Best Local Similarity 69.5%; Pred. NO. 1.2e-20;
Matches 182; Conservative 0; Mismatches 71; Indels 9; Gaps 1;

QY 127 ttacaggagcagcgcaaccatttgcaggagcgaactgtcggagctcaggtgagcagacaga 186
DB 1268 TTGCAGGAGCTGTGACCGCTCTACGACAGAGGCTCTCGAGCTGCGAGCGGAGCAGCTG 1327
QY 187 tccttgagccctccagagagcggcccccacacaggtgtcttggagtcggggaggta 246
DB 1328 CGCGTGGAGCCCTCCAGCAGGAGGCGCTGGAAGAACCTGGGACTCCCGCGGGCA 1387
QY 247 gccaccagggatccgtgggacccgcaaatggtctctacacccctggggcaccacga 306
DB 1388 GCCCCGCGGGGTTCCTTGGGCCCCACACAGCCTCTCCAGCCCTCGGGG----- 1440
QY 307 agcccaagatggtgcaagggtgtgctgttttggaggaagatgacccggtcagctcc 366
DB 1440 -GCCCAAGATGATGCGGACACTCGGCTGCTTGGAGGAGGCTGGACCGGATCGGCTCC 1498
QY 367 tccagtggcctgggctgcaag 388
DB 1499 CTCAGTGGCCTGGGCTGCAACG 1520

RESULT 14
DOGBNPA
LOCUS
DEFINITION
Dog brain natriuretic protein (BNP) gene, complete cds.
ACCESSION
M31777
VERSION
M31777.1 GI:163912
KEYWORDS
Dog DNA, clone D1.
SOURCE
ORGANISM
Canis sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
1 (bases 1 to 1803)
Seilhamer, J.J., Arfsten, A.E., Miller, J.A., Lundquist, P.,
Scarborough, R.M., Lewicki, J.A. and Porter, J.G.
TITLE
Human and canine gene homologs of porcine brain natriuretic peptide
JOURNAL
Biochem. Biophys. Res. Commun. 165, 650-658 (1989)
MEDLINE
90088474
FEATURES
Location/Qualifiers
1..1803
/organism="Canis sp."
/db_xref="taxon:9616"
<365..517
/note="brain natriuretic protein"
join(365..517,740..992,1555..1571)
/note="brain natriuretic protein"
/codon_start=1
/protein_id="AAA30832.1"
/db_xref="GI:163913"
SGLNVAQELLRLDAVSELQAEQLALEPLHRSAPAPAGSTPGVPLAPHDSVLQ
ALRRRSFKMHKSGCFERRLDRLIGLSLGLCNVLRKY"
-intron 518..739
/note="brain natriuretic protein, intron A"
exon 740..992
/number=2
intron 993..1554
/note="brain natriuretic protein, intron B"
exon 1555..>1571
/note="brain natriuretic protein"
/number=3
BASE COUNT 358 a 552 c 526 g 367 t
ORIGIN

Query Match 29.0%; Score 116.4; DB 3; Length 1803;
Best Local Similarity 67.9%; Pred. NO. 1.2e-19;
Matches 178; Conservative 0; Mismatches 81; Indels 3; Gaps 1;

QY 127 ttacaggagcagcgcaaccatttgcaggagcgaactgtcggagctcaggtgagcagacaga 186
DB 734 TTGCAGGAGCTGCTGGGCGCTGTGAAGGACGCGAGTTTCAGAGCTCGAGCGAGCAGTTG 793
QY 187 tccttgagccctccagagagcggcccgctccacaggtgtcttgaagtcccgaggta 246
DB 794 GCCCTGGAAACCCCTGCACCGGAGCCACAGCCCGGAGAGCCCGGAGGCC---GGAGA 850
QY 247 gccaccagggatccgtgggacccgcaaatggtctctacacccctggggcaccacga 306
DB 851 AGCCCCCGTGGGTCTTGCACCCCATGACAGTGTCTCCAGGCCCTGAGAAGACTACGC 910
QY 307 agcccaagatggtgcaagggtgtgctgttttggaggaagatgacccggtacgctcc 366
DB 911 AGCCCCAAGATGATCAAGTCAAGGTGCTTTGGCCGAGGCTGGACCGATCGGCTCC 970
QY 367 tccagtggcctgggctgcaag 388
DB 971 CTCAGTGGCCTGGGCTGCAATG 992

RESULT 15
E05300
LOCUS
DEFINITION
DNA encoding human natriuretic peptide.
ACCESSION
E05300
VERSION
E05300.1 GI:2173490

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KEYWORDS JP 1993207891-A/1.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 96)
AUTHORS Yoshida,N., Shin,M., Teraoka,H., Tamaki,M., Inoue,T. and
Watanabe,K.
TITLE PRODUCTION OF BRAIN NATRIURETIC PEPTIDE
JOURNAL Patent: JP 1993207891-A 1 20-AUG-1993;
SHIONOGI & CO LTD
COMMENT OS Homo sapiens (human)
PN JP 1993207891-A/1
PD 20-AUG-1993
PF 08-MAR-1991 JP 1991043641
PI YOSHIDA NOBUO, SHIN MASARU, TERAOKA HIROSHI, TAMAKI MIKIO, PI
INOUE TAKESHI,
PI WATANABE KUNIO
PC C12P21/06.C07K13/00.C12N1/21.C12N15/16.C12N15/62.C12N15/70, PC
C12P21/02//
PC A61K37/02.A61K37/24.(C12N1/21.C12R1:19).(C12P21/02.C12R1:19);
CC strandedness: Double;
CC topology: Linear;
CC Feature is identified by similarity;
FH Key Location/Qualifiers
FT mat_peptide 1..96
FT Location/Qualifiers
source 1..96
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 19 a 23 c 36 g 18 t
ORIGIN

Query Match 23.9%; Score 96; DB 5; Length 96;
Best Local Similarity 100.0%; Pred. No. 2e-14;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 307 agccccaaagatggtgcaagggtctgtggtcttggagggaagatggaccggatcagctcc 366
|||||
Db 1 AGCCCCAAGATGGTGCAGGGTCTGGCTTTGGGAGGAGATGGACCGGATCAGCTCC 60
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Qy 367 tccagtggcctgggtgcaagtgctgagcgccat 402
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Db 61 TCCAGTGGCTGGGCTGCAAGTGTCTGAGGCGCAT 96
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